

Scoring table:	BLOSUM62	Scored by:	Gapop 10.0 , Gapext 0.5	ALIGNMENTS			
Searched:	127863 seqs, 47026705 residues	Total number of hits satisfying chosen parameters:	127863	RESULT 1			
Minimum DB seq length:	0	Maximum DB seq length:	2000000000	ID ALBU_HUMAN STANDARD; P02768; Q95574; Q13140; Q9P157; Q0QHS3; Q9UJ20;			
Post-processing:	Minimum Match 0%	Maximum Match 100%	Listing first 45 summaries	AC P02768; 095574; Q13140; Q9P157; Q0QHS3; Q9UJ20;			
Database :	SwissProt_41; *			DT 21-JUL-1986 (Rel. 01, Created)			
				DT 01-APR-1990 (Rel. 14, Last sequence update)			
				DT 15-SEP-2003 (Rel. 42, Last annotation update)			
Perfect score:	58	Title:	US-09-845-726A-1_COPY_2_12	DE Serum albumin precursor.			
Sequence:	1 AHKSEVAHREFK 11			GN ALB.			
Scoring table:	BLOSUM62			OS Homo sapiens (Human).			
				ECUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI;			
				OC MAMMALIA; EUOTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.			
				OX NCBI_TAXID=9606;			
				RN [1]			
				RP SEQUENCE FROM N.A., AND VARIANT LYS-420.			
				RX MEDLINE-8616112; PubMed-3009475;			
				RA Manghetti P.P.; Ruffner D.E.; Kuang W.J.; Dennison O.E.; Hawkins J.W.,			
				RA Beattie W.G.; Dugaiczyk A.;			
				RT "Molecular structure of the human albumin gene is revealed by			
				RT nucleotide sequence within q11-22 of chromosome 4.";			
				RL J. Biol. Chem., 261:6747-6757(1986).			
				RN [2]			
				RP SEQUENCE FROM N.A., AND VARIANT GLY-420.			
				RX MEDLINE-8201882; PubMed-6171778;			
				RA Lawn R.M.; Adelman J.; Bock S.C.; Franke A.E.; Houck C.M.,			
				RA Narayan R.C.; Seeburg P.H.; Wilson K.L.;			
				RT "Nucleotide sequence and the encoded amino acids of human serum albumin cDNA and its expression in E. coli.";			
				RT Nucleic Acids Res., 9:6103-6114(1981).			
				RL RN [3]			
				RP SEQUENCE FROM N.A., AND VARIANT GLY-121.			
				RX MEDLINE-82105949; PRO26399.			
				RA Zhang C.; Yu Y.; Zhang S.; Wei H.; Bi J.; Zhou G.; Dong C.; Zai Y.,			
				RA Xu W.; Gao F.; Liu M.; He F.; Zhang Y.; Ouyang S.; Luo L.;			
				RT "Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver.";			
				RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
				[6]			
				RP SEQUENCE FROM N.A., AND VARIANT HIROSHIMA-1 LYS-378.			
				RA Huang M.C.; Wu H.T.;			
				RT "The cDNA sequences of human serum albumin.";			
				RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.			
				RN [7]			
				RP SEQUENCE FROM N.A.			

- [16] RN VARIANT CANTERBURY ASN-337.
RP TISSUE-Liver, and Skeletal muscle;
RX MEDLINE=12479257; PubMed=3828358;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Warner L., Shnemben C.M., Schuler G.D.,
RA Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Mullally S.J.,
RA Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Snailius D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marrs M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [18]

RP SEQUENCE OF 25-609.
RX MEDLINE=776187907; PubMed=1225573;
RA Meloun B., Moravec L., Kosikova V.;
RT "Complete amino acid sequence of human serum albumin.";
RL FEBS Lett. 58:134-137(1975).
RN [19]

RP SEQUENCE OF 25-609.
RA Brown J.R., Shockley P., Behrens P.Q.;
RL (In) Bing D.H. (eds.);
RL The chemistry and physiology of the human plasma proteins, pp.23-40,
RN FEBS Lett. 58:134-137(1975).
RN [20]

RP SEQUENCE OF 1-455 FROM N.A.
RC TISSUE=Liver;
RA Menaya J., Parrilla R., Ayuso M.S.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RN [21]

RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=86140059; PubMed=2419329;
URANO Y., Watanabe K., Sakai M., Tamaoki T.;
RT "The human albumin gene. Characterization of the 5' and 3' flanking
regions and the polymorphic gene transcripts.";
RT Dunn M.J.;
J. Biol. Chem. 261:3244-3251(1986).
RN [22]

RP SEQUENCE OF 222-229.
RX MEDLINE=76257808; PubMed=9550757;
WAHLER J.E.;
RT "Lysine residue 199 of human serum albumin is modified by
acetylsalicylic acid.";
RL FEBS Lett. 66:173-175(1976).
RN [23]

RP SEQUENCE OF 25-44 AND 480-499.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
CORBETT J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
1994.";
RT Electrophoresis 15:1459-1465(1993).
RL [24]

RP DISULFIDE BONDS.
RA Saber M.A., Stockbauer P., Moravek L., Meloun B.;
RT "Disulfide bonds in human serum albumin.";
COLLECT. Czech. Chem. Commun. 42:564-579(1977).
RN [25]

RP BILIRUBIN-BINDING SITE
RX MEDLINE=78186630; PubMed=656055;
JACOBSEN C.;
RA "Lysine residue 240 of human serum albumin is involved in high-affinity binding of bilirubin.";
Biochem. J. 171:453-459(1978).

[17] RN VARIANT NAG-2 AND NAG-3.
RP TARIKAN CANTERBURY ASN-337.
RX MEDLINE=87157744; PubMed=3479777;
RA Brennan S.O., Herbert P., "Albumin Canterbury (313 Lys-->Asn). A point mutation in the second domain of serum albumin.";
RT Biochim. Biophys. Acta 912:191-197(1987).
RN [18]

RP VARIANTS NAG-1; HIR-1; HIR-2 AND TOCHIGI.
RX MEDLINE=89345611; PubMed=2762316;
RA Arai K., Neel J.V.;
RT "Amino acid substitutions in inherited albumin variants from Amerindian and Japanese populations.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987).
RN [19]

RP VARIANTS MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA.
RX MEDLINE=90115905; PubMed=2404284;
RA Arai K., Madison J.J., Huss K., Ishioka N., Satoh C., Fujita M., Neel J.V., Sakurabayashi I., Putnam F.W.;
RT "Point substitutions in Japanese alloalbumins";
RT Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
RN [20]

RP DESCRIPTION OF VARIANT REDHILL.
RX MEDLINE=90115852; PubMed=2104980;
RA Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
RT "Albumin Rachill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of human serum albumin whose precursor has an aberrant signal peptidase cleavage site.";
RT proc. Natl. Acad. Sci. U.S.A. 87:4971-501(1990).
RN [21]

RP VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106.
RX MEDLINE=91062352; PubMed=2247440;
RA Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.;
RA Watkins S., Putnam F.W.;
RT "Mutations in genetic variants of human serum albumin found in Italy.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990).
RL [22]

RP VARIANT VENEZIA.
RX MEDLINE=91296740; PubMed=2068071;
RA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M., Minchiotti L., Porta F.W.,
RA "A donor splice mutation and a single-base deletion produce two carboxyl-terminal variants of human serum albumin.";
RT proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
RN [23]

RP VARIANTS IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KOMAGOME-3 HIS-23;
RX MEDLINE=91296740; PubMed=2068071;
RA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M., Minchiotti L., Porta F.W.,
RA "A donor splice mutation and a single-base deletion produce two carboxyl-terminal variants of human serum albumin.";
RT proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
RN [24]

RP VARIANT CASEBROOK ASN-518.
RX MEDLINE=91316157; PubMed=1859851;
RA Peach R.J., Brennan S.O.;
RA Madison J.J., Araki K., Feld R.D., Kyle R.A., Watkins S., Davis E., Matsuda Y.-I., Amaki I., Putnam F.W.;
RT "Genetic variants of serum albumin in Americans and Japanese.";
RT proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
RN [25]

RP VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
RX MEDLINE=92052189; PubMed=1944142;
RA Galliano M., Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H., Rochi D., Porta F.;
RA "Structural characterization of a glycoprotein variant of human serum albumin: albumin Casebrook (94 Asp-->Asn).";
RT Biochim. Biophys. Acta 1097:49-54(1991).
RN [26]

RP VARIANTS WITH IDENTICAL ELECTROPHORETIC MOBILITY ARE PRODUCED
RX MEDLINE=92190339; PubMed=134703;
RA Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H., Rochi D., Porta F.,
RA "Two alloalbumins with identical electrophoretic mobility are produced

Query Match 100.0%; Score 58; DB 1; Length 609;
 Best Local Similarity 100.0%; pred. No. 0.001;
 Matches 1.1; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
 DR 1111111111
 Db 26 AHKSEVAHRFK 36

RESULT 2

ALBU_RAT

ID ALBU_RAT STANDARD PRT; 608 AA.

AC P02770; P11382;

DR 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serum albumin precursor [Contains: Neurotensin-related Peptide (NRP)].

GN ALB.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.

RN [1] NCBI_TaxID=10116;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE=81223722; PubMed=7017712;

RX Sargent T.D., Yang M., Bonner J.;
 RL Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).

RN [2] Nucleotide sequence of cloned rat serum albumin messenger RNA. ";

RN [2] SEQUENCE OF 1-38, AND PROCESSING.

RX MEDLINE=77249657; PubMed=893447;

RX Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.;
 RL Rat liver pre-proalbumin: complete amino acid sequence of the pre-
 piece. Analysis of the direct translation product of albumin
 messenger RNA.";

RN [3] J. Biol. Chem. 252:6846-6855(1977).

RN [3] SEQUENCE OF 25-222.

RX MEDLINE=78109422; PubMed=564345;

RX Isemura S., Ikenaka T.;

RX "Amino acid sequences of fragments I and II obtained by cyanogen
 bromide cleavage of rat serum albumin.";

RN J. Biochem. 83:35-48(1978).

RN [4] SEQUENCE OF 223-288 AND 512-608.

RX MEDLINE=76260152; PubMed=956149;

RX Isemura S., Ikenaka T.;

RX "Fragments of rat serum albumin by cyanogen bromide cleavage and
 the amino acid sequences of four fragments.";

RN [5] J. Biochem. 79:1183-1196(1976).

RN SEQUENCE OF 166-174.

RX TISSUE=Plasma;

RX MEDLINE=87194805; PubMed=2437111;

RX Carraway R.E., Mitra S.P., Cochrane D.E.;

RX "Structure of a biologically active neurotensin-related peptide
 obtained from a Pepsin-treated albumin(s).";

RN J. Biol. Chem. 262:5968-5973(1987).

RN [6] COPPER-BINDING.

RX MEDLINE=79001617; PubMed=80265;

RX Aoyagi Y., Ikenaka T., Ichida F.;

RX "Copper (II)-binding ability of human alpha-fetoprotein.";

RX Cancer Res. 38:3483-3486(1978).

RN -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
 binding capacity for water, Ca²⁺, Na⁽⁺⁾, K⁽⁺⁾, fatty acids,
 hormones, bilirubin and drugs. Its main function is the regulation
 of the colloid osmotic pressure of blood.

RN -1- FUNCTION: NRP REGULATES FAT DIGESTION, LIPID ABSORPTION, AND
 BLOOD FLOW (POTENTIAL).

RN -1- SUBCELLULAR LOCATION: Secreted.

RN -1- TISSUE SPECIFICITY: Plasma.

-1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 -1- SIMILARITY: Contains 3 albumin domains.

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CC

DR ENBL; V01222; CA324532; 1; -.

DR PIR; A93872; ABRS.

DR HSPP; P02768; 1EFB.

DR InterPro; IPR000364; Serum_albumin.

DR Pfam; PF00273; transport_prot; 3.

DR PRINTS; PRO0802; SERUMALBUMIN.

DR ProDom; PD002486; Serum_albumin; 1.

DR SMART; SM00003; ALBUMIN; 3.

DR PROSITE; PS000212; ALBUMIN; 3.

KW Metal-binding; Lipid-binding; repeat; Signal; Copper.

FT SIGNAL 1 18

FT PROPEP 19 24

FT CHAIN 25 608

FT PEPTIDE 166 174

FT DOMAIN 25 205

FT DOMAIN 212 397

FT DOMAIN 404 595

FT METAL 27 COPPER.

FT DISULFID 77 86

FT DISULFID 99 115

FT DISULFID 114 125

FT DISULFID 148 193

FT DISULFID 192 201

FT DISULFID 224 270

FT DISULFID 269 277

FT DISULFID 289 303

FT DISULFID 302 313

FT DISULFID 340 385

FT DISULFID 384 393

FT DISULFID 416 462

FT DISULFID 461 472

FT DISULFID 485 501

FT DISULFID 500 511

FT DISULFID 538 583

FT DISULFID 582 591

FT VARIANT 262 V > L.

FT CONFLICT 174 174 Y > L (IN REF. 5).

SQ SEQUENCE 608 AA; 68718 MW; 5BB49FA2B2411AB7 CRC64;

Query Match 98.3%; Score 57; DB 1; Length 608;

Best Local Similarity 90.9%; Pred. No. 0.0022; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
 DR 1111111111
 Db 26 AHKSEVAHRFK 36

RESULT 3

ALBU_MACMU

ID ALBU_MACMU STANDARD PRT; 600 AA.

AC Q28522;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serum albumin precursor (Fragment).

GN ALB.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

NCBI_TaxID=9544;

Query Match Score 54; DB 1; Length 69;
Best Local Similarity 81.8%; Pred. No. 0.0082; Gaps 0;
Matches 9; Conservative 2; Mismatches 0; Indexes 0;
Matches 9; Conservative 2; Mismatches 0; Indexes 0;

Oy 1 AHKSEVAHRFK 1.1
Db 27 AHKSEIAHRYK 37

RESULT 5

ALBU_BOVIN
ID ALBU_BOVIN STANDARD; PRT; 607 AA.
AC P02769; 002787; RT
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Allergen Bos d 6).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae;
OX NCBI_TAXID:9913; Bos.
RN [1] RP SEQUENCE FROM N.A.
RA Holowchuk E.W.; Stoltzenborg J.K.; Reed R.G.; Peters T. Jr.;
RN [2] Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
RP SEQUENCE FROM N.A., AND VARIANT THR-214.
RC TISSUE:Liver;
RA Barry T.; Power S.; Gannon F.;
RN [3] Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN [4] RP SEQUENCE FROM N.A., AND VARIANT THR-214.
RP SEQUENCE FROM N.A.,
RA Wu H.T.; Huang M.C.;
RC TISSUE:Liver;
RA Hilger C.; Grigioni F.; de Beaufort C.; Michel G.; Hentges F.;
RN [5] Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
RN [6] RP SEQUENCE OF 1-32.
RA MEDLINE-80024278; PubMed=488109;
RA McGillivray R.T.A.; Chung D.W.; Davie E.W.;
RT "Biosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of preproalbamin.";
RN [7] RL Biochem. 98:477-485(1979).
RN [8] RP SEQUENCE OF 25-424 AND 429-607, AND VARIANT THR-214.
RA Brown J.R.;
RT "Structure of bovine serum albumin.";
RL Fed. Proc. 34:591-591(1975).
RN [9] RP REVISIONS TO 190-195.
RA Brown J.R.;
RL Submitted (APR-1975) to the PIR data bank.
RN [10] RP SEQUENCE OF 402-433.
RX MEDLINE=82023364; PubMed=7283978;
RA Reed R.G.; Putnam F.W.; Peters T. Jr.;
RT "Sequence of residues 400-403 of bovine serum albumin.";
RL Biochem. J. 191:867-868(1980).
RN [11] RP SEQUENCE OF 19-28.
RX MEDLINE=7713407; PubMed=8433354;
RA Patterson J.E.; Geller D.M.;
RT "Bovine microsomal albumin: amino terminal sequence of bovine proalbumin.";
RA Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
RN [12] RP SEQUENCE OF 25-41.
RX MEDLINE=88287456; PubMed=3389500;
RA Hsieh J.C.; Lin F.P.; Tam M.F.;
RT "Electroblotting onto glass-fiber filter from an analytical isoelectrofocusing gel: a preparative method for isolating proteins for N-terminal microsequencing.";
RL Anal. Biochem. 170:1-8(1988).
RN [13] RP SEQUENCE OF 437-451.
RA Valbois F.;
RL Submitted (AUG-1998) to the SWISS-PROT data bank.
RN [14] RP DISULFIDE BONDS.
RA Brown J.R.;
RT "Structure of serum albumin: disulfide bridges.";
RL Fed. Proc. 33:1389-1389(1974).
CC [-] FUNCTION: Serum albumin, the main protein of plasma, has a good bonding capacity for water, Ca(2+), Na(+), K(+) fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
CC [-] SUBCELLULAR LOCATION: Secreted.
CC [-] TISSUE SPECIFICITY: Plasma.
CC [-] SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC [-] SIMILARITY: Contains 3 albumin domains.

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CC DR EMBL: M73991; AAA51411.1; -.
CC DR EMBL: X58988; CAR41735.1; -.
CC DR EMBL: Y17765; CAR7684.1; -.
CC DR EMBL: AF542068; AAN1724.1; -.
CC DR HSPP; P02768; 1E7B.
DR InterPro; IPR000264; Serum albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PRO0802; SERUMALBUMIN.
DR Prodom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen;
KW Polymorphism.
FT SIGNAL 1 18
FT PROPEP 19 8
FT CHAIN 25 24
FT DOMAIN 21 20
FT DOMAIN 21 20
FT DOMAIN 21 20
FT METAL 27 27
FT DISULFID 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 147 192
FT DISULFID 191 200
FT DISULFID 223 269
FT DISULFID 268 276
FT DISULFID 288 302
FT DISULFID 301 312
FT DISULFID 339 384
FT DISULFID 383 392
FT DISULFID 415 461
FT DISULFID 460 471

DR EMBL; XB4842; CAA59279_1; -.

DR PIR; JC4660; S57632.

DR HSSP; P02768; 1E7B.

DR INT-PRO; IPR00264; Serum_albumin.

DR Pfam; PF00273; transport_prot; 3.

DR PRNTS; PR00802; SERUMALBUMIN.

DR PROB002486; serum_albumin; 1.

DR SMART; SM00103; ALBUMIN; 3.

DR PROSTE; PS00212; ALBUMIN; 3.

KW Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.

FT SIGNAL 1 18 BY SIMILARITY.

FT PROPEP 19 24 BY SIMILARITY.

FT CHAIN 25 608 SERUM_ALBUMIN.

FT DOMAIN 25 205 ALBUMIN_1.

FT DOMAIN 212 397 ALBUMIN_2.

FT DOMAIN 404 595 ALBUMIN_3.

FT METAL 27 27 COPPER.

FT DISULFID 77 86 BY SIMILARITY.

FT DISULFID 99 115 BY SIMILARITY.

FT DISULFID 114 125 BY SIMILARITY.

FT DISULFID 148 193 BY SIMILARITY.

FT DISULFID 192 201 BY SIMILARITY.

FT DISULFID 224 270 BY SIMILARITY.

FT DISULFID 269 277 BY SIMILARITY.

FT DISULFID 289 303 BY SIMILARITY.

FT DISULFID 302 313 BY SIMILARITY.

FT DISULFID 340 385 BY SIMILARITY.

FT DISULFID 384 393 BY SIMILARITY.

FT DISULFID 416 462 BY SIMILARITY.

FT DISULFID 461 472 BY SIMILARITY.

FT DISULFID 485 501 BY SIMILARITY.

FT DISULFID 500 511 BY SIMILARITY.

FT DISULFID 538 583 BY SIMILARITY.

FT DISULFID 582 591 BY SIMILARITY.

SQ SEQUENCE 608 AA; 68659 MW; 07E629AC5F60E5F CRC64;

Query Match 82.8%; Score 48; DB 1; Length 608;

Best Local Similarity 80.0%; Pred. No. 0.12;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRF 10

Db 11:1:1:1 26 AHOSEIAHRF 35

RESULT 11

ALBU_PIG ID ALBU_PIG STANDARD; PRT; 605 AA.

AC P08835; Q29018; PRT; 605 AA.

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serum_albumin precursor (fragment).

GN ALB.

OS Sus_scrofa (Pig).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TAXID=9823;

RN [1]

RP SEQUENCE FROM N_A.

RC TISSUE=Liver;

RX MEDLINE-89016582; PubMed=3174440;

RA Baldwin G.S.; Weinstock J.;

RT Nucleotide sequence of porcine liver albumin ";

RL Nucleic Acids Res. 16:9045-9045(1988).

CC -I- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- TISSUE SPECIFICITY: Plasma.

CC -I- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.

CC -I- SIMILARITY: Contains 3 albumin domains.

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DR EMBL; XI2422; CAA30970_1; -.

DR PIR; M36787; AAA30988_1; -.

DR HSSP; P02768; 1E7H.

DR InterPro; IPR000264; Serum_albumin.

DR Pfam; PF00273; transport_prot; 3.

DR PRINTS; PRO0802; SERUMALBUMIN.

DR PRODOM; PD002486; Serum_albumin; 1.

DR SMART; SM00103; ALBUMIN; 3.

DR PROSITE; PS000212; ALBUMIN; 3.

KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.

FT NON_TER 1 1 BY SIMILARITY.

FT SIGNAL 1 <1 BY SIMILARITY.

FT PROPEP 17 22 BY SIMILARITY.

FT CHAIN 23 605 SERUM_ALBUMIN.

FT DOMAIN 23 202 ALBUMIN_1.

FT DOMAIN 209 394 ALBUMIN_2.

FT DOMAIN 401 592 ALBUMIN_3.

FT METAL 31 311 COPPER (BY SIMILARITY).

FT DISULFID 75 84 BY SIMILARITY.

FT DISULFID 97 113 BY SIMILARITY.

FT DISULFID 112 123 BY SIMILARITY.

FT DISULFID 145 190 BY SIMILARITY.

FT DISULFID 189 198 BY SIMILARITY.

FT DISULFID 221 267 BY SIMILARITY.

FT DISULFID 266 274 BY SIMILARITY.

FT DISULFID 286 300 BY SIMILARITY.

FT DISULFID 299 310 BY SIMILARITY.

FT DISULFID 337 382 BY SIMILARITY.

FT DISULFID 381 390 BY SIMILARITY.

FT DISULFID 413 459 BY SIMILARITY.

FT DISULFID 458 469 BY SIMILARITY.

FT DISULFID 482 498 BY SIMILARITY.

FT DISULFID 497 508 BY SIMILARITY.

FT DISULFID 535 580 BY SIMILARITY.

FT DISULFID 579 588 BY SIMILARITY.

FT CONFLICT 562 562 E->D (IN REF. 1; AAA30988).

SQ SEQUENCE 605 AA; 69410 MW; 3E556BODDIALF4F CRC54;

Query Match 81.0%; Score 47; DB 1; Length 605;

Best Local Similarity 80.0%; Pred. No. 0.18;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HKSEVAHRF 11

Db 11:1:1:1 25 YKSETAHRF 34

RESULT 12

ALBU_CHICK ID ALBU_CHICK STANDARD; PRT; 615 AA.

AC P19121;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DE Serum albumin precursor.

GN ALB.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC Gallus.

OX NCBI_TAXID=9031;

RN [1]

RP SEQUENCE FROM N_A.

TISSUE:Liver;
 RC Cassedy A. I.; Salkild C.K.; Baverstock P.; Wallace J.C.;
 RA Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
 RL [2]
 RN SEQUENCE OF 1-28 FROM N.A.
 RX MEDLINE=83161037; PubMed=6187737;
 RX Hache R.J.G.; Wiskocil R.; Yasa M.; Roy R.N.; Lau P.C.K.; Deeley R.G.;
 RA "The 5' noncoding and flanking regions of the avian very low density
 RT apolipoprotein II and serum albumin genes. Homologies with the egg
 RT white protein genes";
 RT Biol. Chem. 258:4556-4564 (1983).
 RL [3]
 RN SEQUENCE OF 19-30.
 RP MEDLINE=781019943; PubMed=911327;
 RA Rosen A.M.; Geller D.M.;
 RR "Chicken microsomal albumin: amino terminal sequence of chicken
 proalbumin";
 RL Biochem. Biophys. Res. Commun. 78:1060-1066(1977).
 CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
 CC binding capacity for water, Ca^{2+} , Na^+ , K^+ , fatty acids,
 CC hormones, bilirubin and drugs. Its main function is the regulation
 CC of the colloidial osmotic pressure of blood.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -1- SIMILARITY: Contains 3 albumin domains.

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CC EMBL; X60688; CAA43098.1; -;
 DR V00381; CRAA23680.1; -;
 DR PIR; S15571; ABCHS.
 DR HSSP; P02768; IETB.
 DR Intero; IPR00264; Serum.albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PRO0802; SERONALBUMIN.
 DR PRODOM; PDO02486; SERONALBUMIN; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00103; ALBUMIN; 3.
 DR PROSITE; PS0212; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 FT SIGNAL; 1 18
 FT PROPEP; 19 23
 FT CHAIN DOMAIN; 24 615
 FT DOMAIN; 216 401
 FT DOMAIN; 408 599
 FT METAL; 30 30
 FT DISULFID; 80 89
 FT DISULFID; 102 118
 FT DISULFID; 117 128
 FT DISULFID; 152 197
 FT DISULFID; 196 205
 FT DISULFID; 228 274
 FT DISULFID; 273 281
 FT DISULFID; 293 307
 FT DOMAIN; 306 317
 FT DISULFID; 344 389
 FT DISULFID; 388 397
 FT DISULFID; 420 466
 FT DISULFID; 465 476
 FT DISULFID; 489 505
 FT DISULFID; 504 515
 FT DISULFID; 542 587
 FT DISULFID; 586 595
 FT CARBOHYD; 500 N-LINKED (GLCNAC, . .) (POTENTIAL).
 FT CONFLICT; 24 24 F->M (IN REF. 3).
 SQ 615 AA; 69918 MW; E59E4BBCAEC06666 CRC64;

Query Match 77.6%; Score 45; DB 1; Length 615;
 Best Local Similarity 77.8%; Pred. No. 0.4%;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HKSEVAHRF 10
 Db 30 HKSEVAHRY 38

RESULT 13
 ALBL_TRASC STANDARD PRT; 40 AA.
 ID ALBL_TRASC
 AC P811188;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 67 kDa serum albumin (Alb-1) (Fragment).
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemy's scripta).
 OC Matzoya; Metaxata; Chordata; Craniata; Vertebrata; Reteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
 OC NCBI_TAXID=34903;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=98103404; PubMed=9440230;
 RA Brown M.A.; Chambers G.K.; Licht, P.;
 RR "purification and partial amino acid sequences of two distinct
 RL albumins from turtle plasma";
 RN [2]
 RP SEQUENCE OF 1-8.
 RX MEDLINE=95309661; PubMed=7789749;
 RA Selcer K.W.; Palmer B.D.;
 RT "Estrogen downregulation of albumin and a 170-kDa serum protein in
 the turtle, Trachemys scripta.;"
 RL Gen. Comp. Endocrinol. 97:340-352(1995).
 CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
 CC binding capacity for water, Ca^{2+} , Na^+ , K^+ , fatty acids,
 CC hormones, bilirubin and drugs. Its main function is the regulation
 CC of the colloidial osmotic pressure of blood.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- MISCELLANEOUS: IN THE RED-EARED SLIDER TURTLE, THERE ARE TWO FORMS
 CC OF ALBUMIN, ALB-1 AND ALB-2.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 DR HSSP; P02768; IETB.
 DR Interpro; IPR00264; Serum_albumin.
 DR Pfam; PF00273; transport_prot; 1.
 DR PROSITE; PS00122; ALBUMIN; PARTIAL.
 KW Metal-binding; Lipid-binding; Copper.
 FT METAL 4
 FT NON_TER 40
 SQ SEQUENCE 40 AA; 4682 MW; 5FC9E9E2789BB0 CRC4;
 Query Match 75.9%; Score 44; DB 1; Length 40;
 Best Local Similarity 77.8%; Pred. No. 0.037%;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HKSEVAHRF 10
 Db 4 HKSEIVHRF 12

RESULT 14
 ALBU_CANFA STANDARD PRT; 608 AA.
 ID ALBU_CANFA
 AC P49822; O77705; Q9T74;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor (Allergen Can f 3).
 GN ALB.
 SQ Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=615; [1]

RN SEQUENCE FROM N.A.
RC STRAIN=Beagle; TISSUE=Liver;
RA Hillger C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Liver; PubMed=10669848;
RX MEDLINE=20148667; PubMed=10669848;

RA Pandjaitan B., Svoboda I., Brandejsky-Pichler F., Rumpold H.,
Valenta R., Spitzrauer S.;
RT "Escherichia coli expression and purification of recombinant dog
albumin, a cross-reactive animal allergen.";
RL J. Allergy Clin. Immunol. 105:279-285(2000).
RN [3]

RP SEQUENCE OF 25-48.
RX MEDLINE=75011422; PubMed=4414013;
RA Dixon J.W., Sarkar B.;
RT "Isolation, amino acid sequence and copper(II)-binding properties of
peptide (1-24) of dog serum albumin.";
RL J. Biol. Chem. 249:5872-5877(1974).
RN RP SEQUENCE OF 25-38.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9804812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
RN RP SEQUENCE OF 215-478 FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=94201492; PubMed=7512102;
RA Spitzrauer S., Schweiger C., Speir W.R., Pandjaitan B., Valent P.,
Muehl S., Ebner C., Scheiner O., Kraut D., Rumpold H.;
RT "Molecular characterization of dog albumin as a cross-reactive
allergen."
RL J. Allergy Clin. Immunol. 93:614-627(1994).
CC -I- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Plasma.
CC -I- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC -I- SIMILARITY: Contains 3 albumin domains.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AJ133489; CAB64067; 1; -.
DR EMBL; Y17737; CAA16841; 1; -.
DR EMBL; S72946; AA30434; 1; -.
DR HSSP; P02768; 1E8B.
DR HSC-2DPAGE; P49B22; DOG.
DR InterPro; IPR00264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTER; PR00802; SERMONALBIRIN.
DR PRODOM; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 24 Gough J., Gossik A., Gozil M., Gossik C., Frazer K.S.,
FT CHAIN 25 608 SERUM ALBUMIN.

FT DOMAIN 25 ALBUMIN 1.
FT DOMAIN 212 ALBUMIN 2.
FT DOMAIN 404 ALBUMIN 3.
FT METAL 27 COPPER (BY SIMILARITY)
FT DISULFID 77 86 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
FT CONFLICT 1 26 MKVTFISLEFLSSAYSRGLYRREA -> MDIT (IN
REF. 2).
FT CONFLICT 146 146 A -> R (IN REF. 2).
FT CONFLICT 206 206 I -> T (IN REF. 2).
FT CONFLICT 349 349 V -> A (IN REF. 2).
FT CONFLICT 359 359 S -> A (IN REF. 1).
FT CONFLICT 448 448 V -> VV (IN REF. 5).
FT CONFLICT 474 474 D -> E (IN REF. 1).
SQ SEQUENCE 608 AA; 6860 MW; 3CFC1C8FF7DDBFC06 CRC64;
Query Match 74.60%; Score 43; DB 1; Length 608;
Best Local Similarity 70.0%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
RBMC_MOUSE STANDARD; PRT; 1002 AA.
ID RBMC_MOUSE STANDARD; PRT; 1002 AA.
AC Q8K4X3; Q8K373; Q8R302; Q9GCS80;
DT 15-SEP-2003 (Rel. 4.2, Created)
DT 15-SEP-2003 (Rel. 4.2, Last sequence update)
DT 15-SEP-2003 (Rel. 4.2, Last annotation update)
DE RNA-binding protein 1.2 (RNA binding motif protein 12) (SH3/WW domain
DE anchor protein in the nucleus) (SWAN).
GN RM12.
OS Mus musculus (Mouse).
OC Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OX NCBI_TAXID=10090;
RN SEQUENCE FROM N.A.
RP Huang C.-H.;
RT "Identification of SWAN as a novel hnRNP-like adaptor protein with
multiple domains and broadly expressed in mammalian tissues.", with
multiple domains and broadly expressed in mammalian tissues.", with
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Head;
RX MEDLINE=22351683; Published=12466851;
RA Okuzaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nakaido I., Osato N., Saito R., Suzuki H., Yamakawa I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.A., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batzloff S., Beisel K.W.,
RA Bradt D., Brusic V., Fletcher C.F., Forrest A., Frazer K.S.,
RA Dalla E., Dragani T.A., Gozil M., Gossik A., Gossik C., Gough J.,
RA Gaasterland T., Garibaldi M., Gossik C., Frazer K.S.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA	Kanai A., Kawahashi Y., Kawassawa Y., Kedzierski R.M., King B.L.,	FT	DOMAIN	430	507	RNA-BINDING (RRM) 2.
RA	Konagaya A., Kurochkin I.V., Lee Y., Lehnard B., Lyons P.A.,	FT	DOMAIN	644	925	PRO-RICH.
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mikici H.,	FT	DOMAIN	656	924	GLY-RICH.
RA	Petrosimyo N., Pillai R., Pontius J.D., Qi D., Ramachandran S.,	FT	DOMAIN	926	1002	RNA-BINDING (RRM) 3.
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,	FT	CONFFLICT	122	122	I -> T (IN REF. 1).
RA	Schneider C., Semple C.A., Setou M., Shimada K.,	FT	CONFFLICT	572	572	N -> S (IN REF. 2;
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,	FT	CONFFLICT	719	719	BAC26338/BAC28911/BAC38017).
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,	FT	CONFFLICT	729	729	G -> S (IN REF. 2; BAC38025).
RA	Wuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,	FT	CONFFLICT	739	739	G -> C (IN REF. 2; BAB30825).
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,	FT	CONFFLICT	757	766	MISSING (IN REF. 2;
RA	Shiraki T., Waki K., Aizawa K., Fukuda S.,	FT	CONFFLICT	762	766	BAB30825/BAC28911/BAC38017).
RA	Hara A., Hashizume W., Imoto K., Ishii Y., Itoh M., Kagawa I.,	FT	CONFFLICT	819	819	MISSING (IN REF. 2; BAC26338).
RA	Miyazaki A., Sakai K., Sesaki D., Shibata K., Shinagawa A.,	FT	CONFFLICT	824	824	G -> GGG (IN REF. 1).
RA	Yasunishi A., Hayashizaki Y.; Birney E., Hayashizaki Y.; Rogers J.,	FT	CONFFLICT	827	827	V -> A (IN REF. 1).
RA	"Analysis of the mouse transcriptome based on functional annotation of full-length cDNAs." ;	FT	CONFFLICT	842	842	V -> G (IN REF. 1).
RA	Nature 420:563-573 (2002). ;	FT	CONFFLICT	849	850	E -> D (IN REF. 1).
RA	[3]	FT	CONFFLICT	907	907	AP -> G (IN REF. 1).
RN	SEQUENCE OF 116-1002 FROM N.A.	SQ	SEQUENCE	1002	AA:	5B560124232F6A49 CRC64;
RC	SEQUENCE=C57BL/6J; TISSUE="breast tumor";					
RC	STRAIN=C57BL/6J; PubMed=12477932;					
RX	MEDLINE=22388257;					
RA	Klauser R.D., Feingold E.A., Grouse L.H., Derge J.G., Derge J.G.,	Qy	Best Local Similarity	63.8%	Score 37;	DB 1;
RA	Klauser R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,	Matches	Local Similarity	72.7%	Pred. No. 27;	Length 1002;
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	8;	Conservative	0;	Mismatches	0;
RA	Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,	Db	1 AHKSEYAHFRK 11			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		11111 111			
RA	Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		598 AHKSEHILHRKK 608			
RA	Brownstein M.J., Usdin T.B., Yoshiaki S., Carninci P., Prange C.,					
RA	Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,					
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,					
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA	Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,					
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,					
RA	Schniech A., Schein J.E., Jones S.J.M., Marra M.A.;					
RA	"Generation and initial analysis of more than 15,000 full-length human					
RA	and mouse cDNA sequences." ;					
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).					
CC	-1- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.					
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DR	EMBL; AF34534; AAH63754; -;					
DR	EMBL; AF393215; AAM73683; -;					
DR	EMBL; AF393216; AAM73684; -;					
DR	EMBL; AK017591; BAB30825; -;					
DR	EMBL; AK029180; BAC26338; -;					
DR	EMBL; AK035014; AAC2811; -;					
DR	EMBL; AK080772; BAC38017; -;					
DR	EMBL; BC026891; AAH76891; ALT_INIT.					
DR	EMBL; BC027810; AAH27810; ALT_INIT.					
DR	MGI; MGI:1922960; Rm12.					
DR	InterPro; IPR000504; RNA_rec_mot.					
DR	Pfam; PF00076; rim; 3.					
DR	SMART; SM00360; RRM; 4.					
DR	PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.					
KW	Nuclear protein; RNA-binding; Repeat.					
FT	DOMAIN 159 256 RNA-BINDING (RRM) 1.					
FT	304 379 RNA-BINDING (RRM) 1.					

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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:23:55 ; Search time 95 Seconds
(without alignments)
29.880 Million cell updates/sec

Title: US-09-845-726a-1_COPY_2_12
Perfect score: 58
Sequence: 1 AHKSEVAHRFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs., 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPRMBL_23:
 1: sp_archaea;*
 2: sp_bacteria;*
 3: sp_fungi;*
 4: sp_human;*
 5: sp_invertebrate;*
 6: sp_mammal;*
 7: sp_mhc;*
 8: sp_organelle;*
 9: sp_phage;*
 10: sp_plant;*
 11: sp_rabbit;*
 12: sp_virus;*
 13: sp_vertebrate;*
 14: sp_unclassified;*
 15: sp_rvirus;*
 16: sp_bacteriaph;*
 17: sp_archeap;*

ALIGNMENTS

RESULT 1
Q9OVA1 PRELIMINARY; PRT; 21 AA.
ID Q9OVA1
AC Q9OVA1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DR 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 49 kDa protein (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Scturognathii; Muridae; Murinae; Rattus.
OC NCTI_TAXID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=93105636; PubMed=1468220;
RA Zhu L.; Crouch R. K.;
RT 'Albumin in the cornea is oxidized by hydrogen peroxide.';
DR HSSP; P02768; 1E7H
DR InterPro; IPR00264; Serum_albumin.
DR PF00273; transport_prot; 1;
SQ SEQUENCE 21 AA; 2429 MW; 26134A3D7CE29FAC CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	58	100.0	21	11	Q9OVA1	Q9oval ratus sp.
2	58	100.0	396	4	Q8TUK7	Q9iuik7 homo sapien
3	57	98.3	20	11	Q9OUX8	Q9qux8 ratus sp.
4	57	98.3	608	5	Q9Vb7	Q9rb7 schistosoma
5	53	91.4	20	2	Q9RAX7	Q9r4x7 mycobacteri
6	52	89.7	40	6	Q9PRA5	Q9ra5 oryctolagus
7	49	84.5	205	11	Q9EG74	Q9eg74 mus musculus
8	49	84.5	608	11	Q8C7H3	Q8c7h3 mus musculus
9	45	77.6	30	13	Q9PRW0	Q9prw0 struthio ca
10	43	74.1	20	6	Q9TQZ6	Q9tqz6 macaca fasc
11	43	74.1	17	6	Q9FR98	Q9pqk4 ureaplasma
12	39.5	68.1	201	16	Q9PQK4	Q8eqm2 oceanobacil
13	38	65.5	152	16	Q8BQM2	Q8i5d0 plasmidium
14	38	65.5	3209	5	Q815D0	Q8yn11 anabena sp
15	37	63.8	93	16	Q8YNT1	Q98nt8 rhizobium 1
16	37	63.8	253	16	Q9P2R8	

RESULT 2
Q8TUK7 PRELIMINARY; PRT; 396 AA.
ID Q8TUK7
AC Q8TUK7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

SEQUENCE; MEDLINE=16273610; PubMed=8690030;	RT	Nucleic Acids Res. 30:3927-3935(2002).
Nicolas M.G., Fujiki K., Murcayama K., Suzuki M.T., Mineki R., Hayakawa M., Yoshikawa Y., Cho F., Kanai A.; "Studies on the mechanism of early onset macular degeneration in cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations of two proteins in the retina.".	RA	DR EMBL; AP004598; BAC13629.1; -.
RT RT	RA	KW Hypothetical protein; Complete proteome.
SEQUENCE 20 AA; 62:21-219(1996); EXP. EYE RES.	RA	SQ SEQUENCE 152 AA; 18357 MW; 5FCAF143BF2D0265 CRC64;
Query Match 65.5%; Score 38; DB 16; Length 152; Best Local Similarity 66.7%; Pred. No. 9.7%; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	Qy	Query Match 65.5%; Score 38; DB 16; Length 152; Best Local Similarity 66.7%; Pred. No. 9.7%; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
2 HKSEVAHFR 10	Db	2 HKSEVAHFR 10 1 : : 19 HKSDLLHRF 27
RESULT 14		
Q815D0 PRELIMINARY; PRT; 3209 AA.	ID	Q815D0 PRELIMINARY; PRT; 3209 AA.
Q815D0; AC 01-MAR-2003 (TREMBLrel. 23, Created)	ID	Q815D0; AC 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	DT	DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE Hypothetical protein.	DE	DE Hypothetical protein.
GN PFL1395C.	GN	OS Plasmodium falciparum ("isolate 3D7").
OS Elaioryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	OS	OC Elaioryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN NCBI_TaxID=36329; [1]	RN	OX NCBI_TaxID=36329; [1]
SEQUENCE FROM N.A.		
RC STRAIN=3D7;	RC	RC STRAIN=3D7;
RX MEDLINE=12255705; PubMed=12368864;	RX	RX MEDLINE=12255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Neilson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallow S.J., Suh B., Petterick J., Anguiano S., Perreira M., Allen J., Selengut J., Haff D., Mather M.W., Valdya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.; "Genome sequence of the human malaria parasite Plasmodium falciparum."	RA	RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Neilson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallow S.J., Suh B., Petterick J., Anguiano S., Perreira M., Allen J., Selengut J., Haff D., Mather M.W., Valdya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.; "Genome sequence of the human malaria parasite Plasmodium falciparum."
RT Nature 419:498-511(2002). DR EMBL; AE014848; AA36365.1; -.	RT	RT Nature 419:498-511(2002). DR EMBL; AE014848; AA36365.1; -.
RT KW Hypothetical protein.	RT	RT KW Hypothetical protein.
RT SQ SEQUENCE 3209 AA; 378904 MW; DA2BBE173C10873 CRC64;	RT	RT SQ SEQUENCE 3209 AA; 378904 MW; DA2BBE173C10873 CRC64;
RESULT 12		
Q9P0K4 PRELIMINARY; PRT; 201 AA.	ID	Q9P0K4 PRELIMINARY; PRT; 201 AA.
Q9P0K4; ID 01-OCT-2000 (TREMBLrel. 15, Created)	ID	Q9P0K4; ID 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DT	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Hypothetical protein UU287.	DE	DE Hypothetical protein UU287.
GN UU287.	GN	OS ureaplasma parvum (Ureaplasma urealyticum biotype 1), Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OC NCBI_TaxID=134821; [1]	OC	OC NCBI_TaxID=134821; [1]
RN RP SEQUENCE FROM N.A.	RN	RN RP SEQUENCE FROM N.A.
RC STRAIN=Secovar 3;	RC	RC STRAIN=Secovar 3;
RA MEDLINE=20500219; PubMed=11048724;	RA	RA MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Leifkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.; "The complete sequence of the mucosal pathogen Ureaplasma urealyticum,"	RA	RA Glass J.I., Leifkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.; "The complete sequence of the mucosal pathogen Ureaplasma urealyticum,"
RT EMBL; AE002125; AAF30596.1; -.	RT	RT EMBL; AE002125; AAF30596.1; -.
RT "The complete sequence of the mucosal pathogen Ureaplasma urealyticum,"	RT	RT "The complete sequence of the mucosal pathogen Ureaplasma urealyticum,"
RT DR EMBL; AE014848; AA36365.1; -.	RT	RT DR EMBL; AE014848; AA36365.1; -.
RT KW Hypothetical protein; Complete proteome.	RT	RT KW Hypothetical protein; Complete proteome.
RT SQ SEQUENCE 201 AA; 23872 MW; FD001911CA4BD7E8 CRC64;	RT	RT SQ SEQUENCE 201 AA; 23872 MW; FD001911CA4BD7E8 CRC64;
RESULT 13		
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Q8YN11; ID 01-MAR-2002 (TREMBLrel. 20, Created)	ID	Q8YN11; ID 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	DT	DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE Hypothetical conserved protein.	DE	DE Hypothetical conserved protein.
GN OB1673.	GN	OS Oceanobacillus illeyensis.
OS Bacterium; Firmicutes; Bactilli; Oceanobacillus.	OS	OC Bacterium; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=182710; [1]	NCBI_TaxID=182710; [1]	NCBI_TaxID=103690; [1]
RP SEQUENCE FROM N.A.	RN	RP SEQUENCE FROM N.A.
RC STRAIN=IRE831 / DSM 14371 / JCM 11309; MEDLINE=21555285; PubMed=11759840;	RX	RC STRAIN=IRE831 / DSM 14371 / JCM 11309; MEDLINE=21555285; PubMed=11759840;
RA Takami H., Takaki Y., Uchiyama I.; "Genome sequence of Oceanobacillus illeyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments."	RA	RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanebe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RT DNA Res 8:205-213(2001).;
RL DR AP003596; BAB76283.1; -;
EMBL; EMBL;
KW Hypothetical protein; Complete proteome.
SEQUENCE 93 AA; 10516 MW; EA46156FB8729D0E CRC64;

Query Match 63.8%; Score 37; DB 16; Length 93;
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 HKSEVAHRF 10
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Db 46 HAADVAHRF 54

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Job time : 98 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: August 29, 2003, 14:24:05 ; Search time 39 Seconds
(without alignments)
27.125 Million cell updates/sec

Title: US-09-845-726A-1_COPY_2_12
Perfect score: 58
Sequence: 1 AHKSEVAHFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext. 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	PIR_76:*
1:	pir1:*
2:	pir2:*
3:	pir3:*
4:	pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	609	1 ABHUS	Serum albumin prec
2	57	98.3	608	1 ABRTS	Serum albumin prec
3	54	93.1	600	2 A47391	Serum albumin prec
4	54	93.1	609	2 JC5938	albumin - Mongolia
5	53	91.4	607	1 ABBOS	Serum albumin prec
6	48	82.8	607	1 ABSHS	Serum albumin prec
7	48	82.8	607	1 ABROS	Serum albumin prec
8	48	82.8	608	2 S57632	Serum albumin prec
9	47	81.0	605	1 ABPCS	Serum albumin prec
10	45	77.6	615	1 ABCHS	Serum albumin prec
11	43	74.1	24	2 S29749	Serum albumin - do
12	40	69.0	30	2 B61511	Serum albumin, mil
13	39.5	68.1	201	2 E89210	Hypothetical prote
14	37	63.8	93	2 AH3778	Hypothetical prote
15	36	62.1	117	2 T30740	Hypothetical prote
16	36	62.1	489	2 AP3594	Sensory transducti
17	36	62.1	719	2 S63392	probable membrane
18	36	62.1	1827	2 T16270	Hypothetical prote
19	35	60.3	155	2 G65489	LSU ribosomal prot
20	35	60.3	320	2 D96750	unknown protein F2
21	35	60.3	672	2 H82143	methyl-accepting C
22	35	60.3	969	2 T23256	hypothetical prote
23	34	58.6	138	2 C84068	Polycyribonucleotide
24	34	58.6	156	2 T49921	ribosomal protein-1
25	34	58.6	200	2 C81282	Hypothetical prote
26	34	58.6	222	2 A97575	Hypothetical prote
27	34	58.6	222	2 A12795	conserved hypothet
28	34	58.6	385	2 C84748	probable integrase
29	34	58.6	391	2 T42407	gephyrin homolog -

ALIGNMENTS

RESULT 1	ABRUS	serum albumin precursor [validated] - human
N: Alternative names: preproalbumin	N: Contains: kinetochin	C: Species: Homo sapiens (man)
C: Date: 29-Jul-1991 #sequence 31-Jan-1997 #text change 17-Mar-2000	C: Accession: A93743; A93936; T39427; I59286; I59313; G01747; S55314; A91420; S06422;	R:Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Majarai, R.C.; see Nucleic Acids Res. 9, 6105-6114, 1981.
A: Title: The sequence of human serum albumin cDNA and its expression in Escherichia coli	A: Reference number: A93743; PMID:82081882; PMID:6171778	A: Accession: A93743
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A: Accession: A93743	A: Accession: A93936; MUID:82105994; PMID:6275391	A: Reference number: A93743
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A: Molecule type: mRNA	A: Cross-references: GB:ML13075; NID:9178330; PIDN:AAA51688.1; PID:9553173	R:Orano, Y.; Watanabe, K.; Sakai, M.; Tamaki, T.
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	J. Biol. Chem. 261, 3244-3251, 1986
A: Molecule type: DNA	A: Molecule type: DNA	A: Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian fami
A: Residues: 1-26 <URA>	A: Residues: 1-26 <URA>	A: Reference number: I59286; MUID:94181575; PMID:8134387
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
A: Molecule type: DNA	A: Molecule type: DNA	A: Reference number: I59313
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
A: Molecule type: DNA	A: Molecule type: DNA	A: Reference number: I59313
A: Residues: 1-26 <URA>	A: Residues: 1-26 <URA>	A: Status: translated from GB/EMBL/DDBJ
A: Cross-references: GB:ML13075; NID:9178330; PIDN:AAA51688.1; PID:9553173	A: Cross-references: GB:S69192; NID:946032; PIDN:AAB30282.1; PID:9546033	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna
R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
A: Molecule type: DNA	A: Molecule type: DNA	A: Reference number: I59313
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
A: Molecule type: DNA	A: Molecule type: DNA	A: Reference number: I59313
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R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
A: Molecule type: DNA	A: Molecule type: DNA	A: Reference number: I59313
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A: Cross-references: GB:ML13075; NID:9178330; PIDN:AAA51688.1; PID:9553173	A: Cross-references: GB:S69192; NID:946032; PIDN:AAB30282.1; PID:9546033	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna
R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
A: Molecule type: DNA	A: Molecule type: DNA	A: Reference number: I59313
A: Residues: 1-26 <URA>	A: Residues: 1-26 <URA>	A: Status: translated from GB/EMBL/DDBJ
A: Cross-references: GB:ML13075; NID:9178330; PIDN:AAA51688.1; PID:9553173	A: Cross-references: GB:S69192; NID:946032; PIDN:AAB30282.1; PID:9546033	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna
R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
A: Molecule type: DNA	A: Molecule type: DNA	A: Reference number: I59313
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A: Cross-references: GB:ML13075; NID:9178330; PIDN:AAA51688.1; PID:9553173	A: Cross-references: GB:S69192; NID:946032; PIDN:AAB30282.1; PID:9546033	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna
R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.	R:Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Putna	Proc. Natl. Acad. Sci. U.S.A. 91, 6756-6780, 1994
A: Status: translated from GB/EMBL/DDBJ	A: Status: translated from GB/EMBL/DDBJ	A: Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox
A: Molecule type: DNA	A: Molecule type: DNA	A: Reference number: I59313
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A: Cross-references: GB:ML		

A; Note: this frame-shift variant is designated albumin Bazzano; four additional variants R; Menaya, J.; Parrilla, R.; Ayuso, M.S.
A; Submitted to the EMBL Data Library, March 1995
A; Reference number: G08892
A; Accession: G01747
A; Status: translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-120, G-, 122-455 <MEN>
A; Cross-references: EMBL:U22461; NID:9763428; PID:9763431
R; Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.Q.
A; Title: Complete amino acid sequence of human serum albumin.
A; Reference number: A91420; MUID:76187907; PMID:1225573
A; Accession: A91420
A; Molecule type: protein
A; Residues: 19-27 <LED>
R; Meljou, B.; Moravek, L.; Kostka, V.
FEBS Lett. 58, 134-137, 1975
A; Title: Complete amino acid sequence of human serum albumin.
A; Reference number: A91420; MUID:76187907; PMID:1225573
A; Accession: A91420
A; Molecule type: protein
A; Residues: 25-117, EQ ,120-154, 'Q', 155-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A' ,395-
R; Roehr, U.; Spitek, G.; Tripler, D.
Justus Liebigs Ann. Chem. 9, 881-884, 1988
A; Title: Isolation and structure elucidation of middle-molecular weight peptides from ur
A; Reference number: S06422
A; Note: this paper is in German, with an English abstract
A; Molecule type: protein
A; Residues: 25-48 <ROE>
R; Finch, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
Arch. Biochem. Biophys. 305, 595-599, 1993
A; Title: Mass spectrometric identification of modifications to human serum albumin treat
A; Reference number: S36882; MUID:93384321; PMID:8373198
A; Accession: S36882
A; Molecule type: protein
A; Residues: 45-67;141-160;311-337;469-490;570-581 <FIN>
R; Kausler, E.; Spittel, G.
Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
A; Title: Bruchstuecke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmol
A; Reference number: S17599; MUID:9216241; PMID:1772598
A; Molecule type: protein
A; Residues: 25-54;354-357;431-447 <KAU>
R; Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A; Title: Structures of histamine-releasing peptides formed by the action of acid proteas
A; Reference number: A45800; MUID:89341406; PMID:2474609
A; Accession: A45800
A; Molecule type: protein
A; Residues: 166-173 <CAR>
R; Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; Wa
Biol. Biophys. Res. Commun. 136, 983-988, 1986
A; Title: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-tre
A; Reference number: A03239; MUID:86242180; PMID:3087332
A; Accession: A03239
A; Molecule type: protein
A; Residues: 166-173 'I' <MOG>
R; Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, S
Proc. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
A; Title: Mutations in genetic variants of human serum albumin found in Italy.
A; Reference number: A38255; MUID:91062352; PMID:2247440
A; Accession: C38255
A; Molecule type: protein
A; Residues: 76-111 <GAL1>
A; Accession: B38255
A; Molecule type: protein
A; Residues: 82-105, 'K', 107-110 <GAL2>
A; Note: this variant is designated albumin Vibo Valentia
A; Accession: A38255
A; Molecule type: protein

A; Residues: 76-83, 'K', 85-106 <GAL3>
A; Note: this variant is designated albumin Torino
R; Minchietti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
Eur. J. Biochem. 214, 437-444, 1993
A; Title: The structural characterization and bilirubin-binding properties of albumin
A; Reference number: S33298; MUID:9329504; PMID:8513793
A; Accession: S33298
A; Molecule type: protein
A; Residues: 25-263, 'E', 265-281 <MIN1>
A; Note: this variant is designated albumin Herborn
R; Minchietti, L.; Galliano, M.; Zapponi, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Por
Biophys. Acta 1119, 232-238, 1992
A; Title: Two alloalbumins with identical electrophoretic mobility are produced by dif
A; Reference number: S21078; MUID:9190239; PMID:1347703
A; Accession: S21078
A; Molecule type: protein
A; Residues: 354-356, 'K', 358-378 <MIN2>
A; Note: this variant is designated albumin Sondrio; another variant Paris-2 is report
R; He, X.M.; Carter, D.C.
Nature 358, 209-215, 1992
A; Title: Atomic structure and chemistry of human serum albumin.
A; Reference number: A46756; MUID:92334427; PMID:91630489
A; Content: annotation; X-ray crystallography, 2.8 angstroms
R; Brown, J.R.; Shockley, P.; Behrens, P.O.
in The Chemistry and Physiology of the Human Plasma Proteins, Bing, D.H., ed., pp.23-
A; Content: annotation; A94442
A; Content: annotation; three-dimensional structure and disulfide bonds
R; Saber, M.A.; Stockbauer, P.; Moravek, L.; Meloun, B.
Collect. Czech. Chem. Commun. 42, 564-579, 1977
A; Title: Disulfide bonds in human serum albumin.
A; Content: annotation; disulfide bonds
R; Jacobsen, C.
Biochem. J. 171, 453-459, 1978
A; Title: Lysine residue 240 of human serum albumin is involved in high-affinity bindi
A; Reference number: A90399; MUID:78186630; PMID:656055
A; Content: annotation; bilirubin-binding site
R; Peters, T.; Reed, R.G.
in Albumin: Structure, Biosynthesis, Function, Peters, J., and Sjoholm, I., eds., 11-
A; Reference number: A9030
A; Content: annotation; conformation and active sites.
A; Reference number: A94408
A; Content: annotation; binding sites
R; Harper, M.E.; Dugaliczyk, A.
Am. J. Hum. Genet. 35, 565-572, 1983
A; Title: Linkage of the evolutionary-related serum albumin and alpha-fetoprotein ge
A; Reference number: A9028; PMID:8327982; PMID:619271
A; Content: annotation; gene position
R; Walker, J.E.
FEBS Lett. 66, 173-175, 1976
A; Title: Lysine residue 199 of human serum albumin is modified by acetylsalicyclic ac
A; Reference number: A46755; MUID:76257808; PMID:955075
A; Content: annotation
A; Note: the nonenzymatic transfer of an acetyl group from aspirin (acetyl salicyclic a
R; Bonney, J.P.; Fonda, M.L.; Feldhoff, R.C.
FEBS Lett. 298, 266-268, 1992
A; Title: Identification of Lys(190) as the primary binding site for pyridoxal 5'-phos
A; Reference number: A56294; MUID:92183881; PMID:1544460
A; Content: annotation
A; Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; 1
atase activity
C; Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized
lirubin, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (we
C; Comment: A large number of variants of human serum albumin have been described.
C; Genetics:
A; Gene: GDB:ALB
A; Cross-references: GDB:118990; OMIM:103600
A; Map position: 4q11-4q13
A; Superfamily: serum albumin; serum albumin repeat homology
C; Keywords: carrier protein; duplication; metal binding; phosphoprotein; plasma; pyri
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 19-24/Domain: propeptide #status experimental <PRO>
F; 25-60/Domain: serum albumin #status experimental <PRO>
F; 29-202/Domain: serum albumin repeat homology <SA1>

F;166-174/Product: kinetensin #status experimental <KIP>
 F;221-394/Domain: serum albumin repeat homology <SA2>
 F;413-592/Domain: serum albumin repeat homology <SA3>
 F;27-86 99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385 ,384-393, 4
 F;214/Binding site: copper (His) #status Predicted
 F;214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 100.0%; Score 58; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.004%;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
 Db 1111111111
 26 AHKSEVAHRFK 36

RESULT 2 ABRTS

serum albumin precursor - rat
 N;Alternate names: preproalbumin
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-May-1979 #sequence revision 31-May-1979 #text_change 22-Jun-1999
 C;Accession: A93872; A92211; A91946; A91940; C45800; 157521; A03233

A;Title: Nucleotide sequence of cloned rat serum albumin messenger RNA.
 A;Reference number: A93872; MUID:81223722; PMID:701772

A;Molecule type: mRNA
 A;Accession: A93872

A;Residues: 1-608 <SAR>
 A;Cross-references: GB:V011222; GB:A92211; PID:CAA24532.1; PID:g556228

R;Strauss, A.W.; Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
 J. Biol. Chem. 252, 6846-6855, 1977

A;Reference number: A92211; MUID:77249657; PMID:893447

A;Note: Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece. Analysis
 A;Reference number: A92211; MUID:81223722; PMID:701772

A;Molecule type: protein
 A;Residues: 1-38 <STR>
 R;Iseamura, S.; Ikenaka, T.
 J. Biochem. 83, 35-48, 1978

A;Title: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage
 A;Reference number: A91946; MUID:78103429; PMID:564345

A;Accession: A91946

A;Molecule type: protein
 A;Residues: 25-222 <IS1>
 R;Iseamura, S.; Ikenaka, T.
 J. Biochem. 79, 1183-1196, 1976

A;Title: Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino acid sequence
 A;Reference number: A91940; MUID:76260153; PMID:956149

A;Accession: A91940

A;Molecule type: protein
 A;Residues: 223-288;572-608 <IS2>
 A;Note: 262-Leu was also found
 R;Aoayagi, Y.; Ikenaka, T.; Ichida, F.
 Cancer Res. 38, 3483-3486, 1978

A;Title: Copper(II)-binding ability of human alpha-fetoprotein.
 A;Reference number: A90758; MUID:79001617; PMID:80265

A;Content: annotation: copper binding
 R;Carraway, R.B.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
 J. Immunol. 143, 1680-1684, 1989

A;Title: Structures of histamine-releasing peptides formed by the action of acid proteases
 A;Reference number: A45800; MUID:89341406; PMID:2474609

A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 166-173 <CAR>
 R;Heard, J.

Mol. Cell. Biol. 7 2425-2434, 1987

A;Title: Determinants of rat albumin promoter tissue specificity analyzed by an improved
 A;Reference number: 157621; MUID:87286876; PMID:3475566

A;Accession: 157621

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
 A;Residues: 1-5 <RES>
 A;Cross-references: GB:ML6825; PIDN:AAA40712.1; PID:g554412

C;Superfamily: serum albumin repeat homology
 C;Species: carrier protein; duplication; metal binding; plasma
 F;1-18/Domain: signal sequence #status experimental <SIG>
 F;19-24/Domain: propeptide #status experimental <PRO>
 F;25-608/Product: serum albumin #status experimental <MAT>
 F;29-202/Domain: serum albumin repeat homology <SA1>
 F;221-394/Domain: serum albumin repeat homology <SA2>
 F;413-592/Domain: serum albumin repeat homology <SA3>
 F;27/Binding site: copper (His) #status experimental <MAT>
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Qy 1 AHKSEVAHRFK 11
 Db 1111111111
 26 AHKSEVAHRFK 36

RESULT 3

serum albumin precursor - rhesus macaque
 C;Species: Macaca mulatta (rhesus macaque)
 C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
 C;Accession: A47391

R;Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam, Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993

A;Title: cDNA and protein sequence of polymorphic macaque albumins that differ in b1
 A;Reference number: A47391; MUID:32111971; PMID:8460152

A;Contents: B/B homozygote
 A;Accession: A47391
 A;Status: preliminary
 A;Molecule type: tRNA; protein
 A;Residues: 1-600 <WAT>
 A;Cross-references: GB:M9463; PIDN:AAA36906.1; PID:g342295

A;Experimental source: liver
 A;Note: sequence extracted from NCBI backbone (NCBIP:128280, NCBIP:128281)

C;Superfamily: serum albumin repeat homology
 C;Species: serum albumin; serum albumin repeat homology <SA1>
 F;21-3-386/Domain: serum albumin repeat homology <SA2>
 F;405-584/Domain: serum albumin repeat homology <SA3>

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 Best Local Similarity 100.0%; Pred. No. 0.023%;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HKSEVAHRFK 11
 Db 1111111111
 19 HKSEVAHRFK 28

RESULT 4

serum albumin - Mongolian jird
 C;Species: Meriones unguiculatus (Mongolian jird)
 C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 19-May-2000

R;Toshiida, K.; Sero-Oshshima, A.; Sinohara, H.
 DNA Res. 4, 351-354, 1997

A;Title: Sequencing of cDNA encoding serum albumin and its extrahepatic synthesis in
 A;Reference number: JC5838; MUID:3811663; PMID:9455485

A;Accession: JC5838
 A;Molecule type: mRNA
 A;Residues: 1-609 <YOS>

A;Cross-references: DDBJ:AB006197; NID:g231727; PIDN:BAA21765.1; PID:g231728

A;Experimental source: liver
 C;Superfamily: serum albumin repeat homology <SA2>
 F;222-395/Domain: serum albumin repeat homology <SA2>

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 Matches 9; Conservative 2; Indels 0;

Qy 1 AHKSEVAFRK 11
 Db 27 AHKSEIAHRYK 37

Submitted to the Atlas, April 1975
 A; Reference number: A91458
 A; Accession: A91458
 A; Molecule type: protein
 A; Residues: 25-41, H, 43-57, 59-64 <SPR>
 A; Title: Structure of a biologically active neurotensin-related peptide obtained from pe
 A; Reference number: A26693; MUID:87194805; PMID:243711
 A; Accession: A45800
 A; Molecule type: protein
 A; Residues: 163-172 <CAR>
 R; Carrauay, R.E.; Mitra, S.P.; Cochrane, D.E.
 J. Biol. Chem. 262, 5968-5973, 1987
 A; Title: Structure of histamine-releasing peptides formed by the action of acid proteas
 A; Reference number: A45800; MUID:89341406; PMID:2474609
 A; Accession: A26693
 A; Molecule type: protein
 A; Residues: 165-172, 'L, <CA2>
 R; Carrauay, R.G.; Putnam, F.W.; Peters Jr., T.
 Biochem. J. 191, 867-868, 1980
 A; Title: Sequence of residues 400-403 of bovine serum albumin.
 A; Reference number: A90309; MUID:82023364; PMID:7283978
 A; Molecule type: protein
 A; Residues: 402-433 <REE>

R; Brown, J.R. Fed. Proc. 34, 591, 1975
 A; Title: Structure of bovine serum albumin.
 A; Reference number: A91458
 A; Accession: A91458
 A; Molecule type: protein
 A; Residues: 25-41, H, 43-117, 'EQ', 120-179, 181-189, 'E', 191-194, 'A', 196-213, 'T', 215-288
 Submitted to the Atlas, April 1975
 A; Reference number: A94551
 A; Accession: A94551
 A; Molecule type: protein
 A; Residues: 190-195 <BR2>
 R; Brown, J.R. Fed. Proc. 33, 1389, 1974
 A; Reference number: A91457
 A; Accession: A91457
 A; Molecule type: protein
 A; Residues: 190-195 <BR2>
 R; Werlein, R.C.; Offord, R.E.; Rose, K. Biochem. J. 302, 907-911, 1994
 A; Title: Preparation and characterization of novel substrates of insulin proteinase (A; Reference number: S55232; MUID:95031935; PMID:7945219
 A; Accession: S55232
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 529-536, 569-572 <WERS>
 C; Superfamily: serum albumin; serum albumin repeat homology
 C; Keywords: carrier protein; copper binding; duplication; plasma
 F; 1-18/Domain: signal sequence #status experimental <PRO>
 F; 19-24/Domain: propeptide #status experimental <PRO>
 F; 25-60/Domain: product; serum albumin #status experimental <MPY>
 F; 29-30/Domain: serum albumin repeat homology <SA1>
 F; 220-393/Domain: serum albumin repeat homology <SA2>
 F; 412-591/Domain: serum albumin repeat homology <SA3>
 F; 27/Binding site: copper (His) #status predicted
 F; 77-86, 99-115, 114-125, 147-192, 191-200, 223-269, 268-302, 301-312, 339-384, 383-39

Query Match 91.4%; Score 53; DB 1; Length 607;
 Best Local Similarity 90.0%; Pred. No. 0.035; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HKSEVAHRFK 11
 Db 27 HKSEIAHRYK 36

RESULT 6
 ABSHS
 serum albumin precursor - sheep
 C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C; Date: 31-dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C; Accession: S06336
 R; Brown, W.M.; Dzieglewska, K.M.; Foreman, R.C.; Saunders, N.R.
 Nucleic Acids Res. 17, 10495, 1989
 A; Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.
 A; Reference number: S06936; MUID:90098888; PMID:2602160
 A; Accession: S06336
 A; Molecule type: mRNA
 A; Residues: 1-607

 A; Cross-references: EMBL:X17055; NID:91386; PID:9A34903.1; PID:91387
 C; Comment: Serum albumin is synthesized in the liver as preprotein. It binds copper
 teroid hormones (weak bonds with these hormones promote their transfer across the mem
 C; Superfamily: serum albumin repeat homology <SA1>
 C; Keywords: carrier protein; duplication; metal binding; plasma
 F; 1-18/Domain: signal sequence #status predicted <PRO>
 F; 19-24/Domain: propeptide #status predicted <PRO>
 F; 25-60/Domain: product; serum albumin #status predicted <MPY>
 F; 29-30/Domain: serum albumin repeat homology <SA1>
 F; 220-393/Domain: serum albumin repeat homology <SA2>
 F; 412-591/Domain: serum albumin repeat homology <SA3>
 F; 27/Binding site: copper (His) #status predicted
 F; 77-86, 99-115, 114-125, 147-192, 191-200, 223-269, 268-302, 301-312, 339-384, 383-39
 F; 263/Binding site: bilirubin (lys) #status predicted

A;Residues: 1-28 <HAC>	Query Match	69.0%	Score 40;	DB 2;	Length 30;
A;Cross-references: GB:V00381; PIDN:CAA23680.1; PMID:963038	Best Local Similarity	63.6%	Pred. No. 0.44;		
R;Rosen, A.M.; Geller, D.M.	Matches	7;	Mismatches	2;	Indels 0;
Biochem. Biophys. Res. Commun. 78, 1060-1066, 1977	Conservative				Gaps 0;
R;Title: Chicken microalbumin: amino terminal sequence of chicken proalbumin.					
R;Reference number: A13451; MUID:78019343; PMID:911327	Qy	1 AHKSEVAHRK 11			
R;Accession: A13451	Db	1 : : : 2 AQKSELGHRYK 12			
R;Molecule type: protein					
R;Residues: 19-23, 'M', 25-30 <ROS>					
C;Comment: Serum albumin is synthesized in the liver as proalbumin. It binds copper, mones (weak bonds with these hormones promote their transfer across the membranes), thyro-	RESULT 13				
C;Superfamily: serum albumin; serum albumin repeat homology	E82910				
C;Keywords: carrier protein; duplication; metal binding; plasma	hypothetical protein UU287 [imported] - Ureaplasma urealyticum				
F;1-18/Domain: signal sequence #status predicted <SIG>	C;Species: Ureaplasma urealyticum				
F;19-26/Domain: propionate #status predicted <PRO>	C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000				
F;27-613/Product: serum albumin #status Predicted <MAT>	C;Accession: E82910				
F;32-206/Domain: serum albumin repeat homology <SA1>	R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.				
F;325-398/Domain: serum albumin repeat homology <SA2>	submitted to GenBank, February 2000				
F;417-596/Domain: serum albumin repeat homology <SA3>	A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a				
F;80/Binding site: copper (His) #status predicted	A;Reference number: A82870				
F;80-89,102-118,117-128,152-197,196-205,228-274,281,293-307,306-317,344-389,388-397,	A;Accession: E82910				
Qy	2 HKSEVAHRF 10				
Query Match	Score 45;	DB 1;	Length 615;		
Best Local Similarity	77.8%	Pred. No. 1.2;			
Matches	7;	Mismatches 2;	Indels 0;	Gaps 0;	
Db	30 HKSEIAHRY 38				
RESULT 11					
S29749	Query Match	68.1%	Score 39.5;	DB 2;	Length 201;
serum albumin - dog	Best Local Similarity	52.6%	Pred. No. 4.1;		
C;Species: Canis lupus familiaris (dog)	Matches	10;	Mismatches 0;	Indels 9;	Gaps 1;
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999	Qy	2 HKS-----EVRAHFRK 11			
C;Accession: S29749	Db	1 : 2 HKSSSLYLTDDEVRAHFRK 97			
R;Dixon, J.W.; Sarkar, B.	RESULT 14				
J. Biol. Chem. 249, 5672-5677, 1974	AH2378				
A;Title: Isolation, amino acid sequence and copper(II)-binding properties of peptide (1-	hypothetical protein asr4584 [imported] - Nostoc sp. (strain PCC 7120)				
A;Reference number: S29749	C;Species: Nostoc sp. PCC 7120				
A;Accession: S29749	C;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. Strain PCC 7120				
A;Status: Preliminary	C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002				
A;Molecule type: protein	C;Accession: AH2378				
A;Residues: 1-24 <DIX>	R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriku-				
C;Superfamily: serum albumin; serum albumin repeat homology	Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata				
Query Match	DNA Res. 8, 205-213, 2001				
Best Local Similarity	A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium				
Matches	A;Reference number: AB1807; MVID:21595285; PMID:11759840				
Qy	A;Accession: AH2378				
1 AHKSEVAHRF 10	A;Status: preliminary				
1 : : : 2 AKSEIAHRY 11	A;Molecule type: DNA				
Db	A;Residues: 1-93 <KUR>				
RESULT 12	A;Cross-references: GB:BA000019; PIDN:BAB76283.1; PID:917133720; GSPDB:GN00179				
B61511	A;Experimental source: strain PCC 7120				
B61511	C;Genetics:				
B61511	A;Gene: asr4584				
B61511	Query Match	63.8%	Score 37;	DB 2;	Length 93;
B61511	Best Local Similarity	66.7%	Pred. No. 5.5;		
B61511	Matches	6;	Mismatches 2;	Indels 1;	Gaps 0;
B61511	Conservative				
B61511	Qy	2 HKSEVAHRF 10			
B61511	Db	46 : 46 HADVAHFR 54			
B61511	RESULT 15				
B61511	T30740				
B61511	hypothetical protein 138R - Molluscum contagiosum virus 1				
B61511	N;Alternate names: MC138R				
B61511	C;Species: Molluscum contagiosum virus 1				
B61511	C;Keywords: milk				
B61511	C;Superfamily: serum albumin; serum albumin repeat homology				

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C;Accession: T30740
R;Senkevich, T.G.; Bigert, J.J.; Sisler, J.R.; Koordin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A;Reference number: 220876; MUID:96325455; PMID:8670425
A;Accession: T30740
A;Status: preliminary; translated from GB/EMBL/DDB/J
A;Molecule type: DNA
A;Residues: 1-117 <SPRN>
A;Cross-references: EMBL:060315; PIDN: AAC552666.1
C;Genetics:
A;Note: MC138R
C;Superfamily: variola major virus 6R protein

Query Match 62.1%; Score 36; DB 2; Length 117;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AHKSEVAFHR 9
Db 1111 111
24 AHKSAFAHR 32

Search completed: August 29, 2003, 14:29:28
Job time : 40 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:27:05 ; Search time 24 Seconds

(without alignments)
13.562 Million cell updates/sec

Title: US-09-845-726A-1_COPY_2_12
Perfect score: 58

Sequence: 1 AHKSEVAHFRK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141812 seqs, 29589763 residues

Total number of hits satisfying chosen parameters:

141812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:
1: /cn2_6_ptodata/2/paa/PCT_NEW_COMBO.PEP:
2: /cn2_6_ptodata/2/paa/US06_NEW_COMBO.PEP:
3: /cn2_6_ptodata/2/paa/US07_NEW_COMBO.PEP:
4: /cn2_6_ptodata/2/paa/US08_NEW_COMBO.PEP:
5: /cn2_6_ptodata/2/paa/US09_NEW_COMBO.PEP:
6: /cn2_6_ptodata/2/paa/US10_NEW_COMBO.PEP:
7: /cn2_6_ptodata/2/paa/US60_NEW_COMBO.PEP:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	54	6 US-10-273-573-10524	Sequence 10524, A
2	58	100.0	76	6 US-10-273-573-5999	Sequence 5999, AP
3	58	100.0	133	6 US-10-273-573-5979	Sequence 5979, AP
4	58	100.0	134	6 US-10-273-573-5922	Sequence 5922, AP
5	58	100.0	156	6 US-10-273-573-5921	Sequence 5921, AP
6	58	100.0	192	6 US-10-273-573-5924	Sequence 5924, AP
7	58	100.0	214	6 US-10-273-573-5933	Sequence 5933, AP
8	58	100.0	289	6 US-10-273-573-5569	Sequence 5569, AP
9	58	100.0	401	6 US-10-273-573-5925	Sequence 5925, AP
10	58	100.0	520	6 US-10-273-573-5926	Sequence 5926, AP
11	58	100.0	550	6 US-10-273-573-5927	Sequence 5927, AP
12	58	100.0	585	1 PCT-US03-18896-26	Sequence 26, Appl
13	58	100.0	585	1 PCT-US03-19902-3	Sequence 3, Appl
14	58	100.0	585	6 US-10-462-262-26	Sequence 26, Appl
15	58	100.0	585	6 US-10-602-141-3	Sequence 3, Appl
16	58	100.0	585	6 US-10-424-99-11	Sequence 11, Appl
17	58	100.0	585	6 US-10-425-000-31	Sequence 31, Appl
18	58	100.0	604	6 US-10-408-765A-55	Sequence 55, Appl
19	58	100.0	609	6 US-10-408-765A-2	Sequence 2, Appl
20	58	100.0	609	6 US-10-609-346-12	Sequence 12, Appl
21	58	100.0	609	7 US-80-490-890-752	Sequence 752, Appl
22	58	100.0	609	7 US-60-490-419-1	Sequence 1, Appl
23	58	100.0	609	7 US-60-490-149-1	Sequence 1, Appl
24	58	100.0	672	6 US-10-424-999-15	Sequence 15, Appl
25	58	100.0	672	6 US-10-425-000-35	Sequence 35, Appl
26	58	100.0	674	6 US-10-424-999-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-273-573-10524
; Sequence 10524, Application US/10273573

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE NUMBER: 2127-066
; CURRENT APPLICATION NUMBER: US/10/273-573
; CURRENT FILING DATE: 2003-10-18
; PRIORITY NUMBER: 09/522, 929
; PRIOR FILING DATE: 2000-04-18
; PRIORITY NUMBER: 09/770, 160
; PRIORITY NUMBER: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO: 10524
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-573-10524

Query Match 100.0% ; Score 58; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHFRK 11
Db 21 AHKSEVAHFRK 31

RESULT 2
US-10-273-573-5999
; Sequence 5999, Application US/10273573

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE NUMBER: 2127-066
; CURRENT APPLICATION NUMBER: US/10/273-573
; CURRENT FILING DATE: 2003-10-18
; PRIORITY NUMBER: 09/522, 929
; PRIOR FILING DATE: 2000-04-18
; PRIORITY NUMBER: 09/770, 160
; PRIORITY NUMBER: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO: 5999
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-10-273-573-5999
Query Match    100.0%; Score 58; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Other INFORMATION: Serum albumin family domain identified by PFam, accession US-10-273-573-5922, PFam score of -21.7

Qy      1 AHKSEVYAHRFK 11
Db      37 AHKSEVYAHRFK 47

RESULT 3
US-10-273-573-5979
: Sequence 5979, Application US/10273573
: GENERAL INFORMATION:
:   APPLICANT: Hyseq, Inc
:   FILE REFERENCE: 21272-066
:   CURRENT APPLICATION NUMBER: US/10/273, 573
:   CURRENT FILING DATE: 2002-10-18
:   PRIOR APPLICATION NUMBER: 09/522, 929
:   PRIOR FILING DATE: 2000-04-18
:   PRIOR APPLICATION NUMBER: 09/770, 160
:   NUMBER OF SEQ ID NOS: 10994
:   SOFTWARE: Custom
:   SEQ ID NO: 5979
:   LENGTH: 133
:   TYPE: PRT
:   ORGANISM: Homo sapiens
:   FEATURE:
:     NAME/KEY: DOMAIN
:     LOCATION: (112)..(127)
:   OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX, accession number PR00802A, p-value=2.324e-14, raw score of 12.17
:   FEATURE:
:     NAME/KEY: DOMAIN
:     LOCATION: (30)..(132)
:   OTHER INFORMATION: Serum albumin family domain identified by PFam, accession number PR00802A, p-value=2.8e-10, PFam score of 47.6
:   FEATURE:
:     NAME/KEY: misc_feature
:     LOCATION: (1)..(133)
:   OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-273-573-5979

Query Match    100.0%; Score 58; DB 6; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.0002; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Other INFORMATION: Serum albumin family domain identified by PFam, accession US-10-273-573-5922, PFam score of 100.3

Qy      1 AHKSEVYAHRFK 11
Db      28 AHKSEVYAHRFK 38

RESULT 4
US-10-273-573-5922
: Sequence 5922, Application US/10273572
: GENERAL INFORMATION:
:   APPLICANT: Hyseq, Inc
:   FILE REFERENCE: 21272-066
:   CURRENT APPLICATION NUMBER: US/10/273, 573
:   CURRENT FILING DATE: 2002-10-18
:   PRIOR APPLICATION NUMBER: 09/522, 929
:   PRIOR FILING DATE: 2000-04-18
:   PRIOR APPLICATION NUMBER: 09/770, 160
:   NUMBER OF SEQ ID NOS: 10994
:   SOFTWARE: Custom
:   LENGTH: 134
:   TYPE: PRT
:   SEQ ID NO: 5922

Query Match    100.0%; Score 58; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.0002; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Other INFORMATION: Serum albumin family domain identified by PFam, accession US-10-273-573-5922, PFam score of -21.7

Qy      1 AHKSEVYAHRFK 11
Db      56 AHKSEVYAHRFK 66

RESULT 5
US-10-273-573-5921
: Sequence 5921, Application US/10273573
: GENERAL INFORMATION:
:   APPLICANT: Hyseq, Inc
:   FILE REFERENCE: 21272-066
:   CURRENT APPLICATION NUMBER: US/10/273, 573
:   CURRENT FILING DATE: 2002-10-18
:   PRIOR APPLICATION NUMBER: 09/522, 929
:   PRIOR FILING DATE: 2000-04-18
:   PRIOR APPLICATION NUMBER: 09/770, 160
:   NUMBER OF SEQ ID NOS: 10994
:   SOFTWARE: Custom
:   SEQ ID NO: 5921
:   LENGTH: 156
:   TYPE: PRT
:   ORGANISM: Homo sapiens
:   FEATURE:
:     NAME/KEY: DOMAIN
:     LOCATION: (120)..(135)
:   OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX, accession number PR00802A, p-value=1.000e-19, raw score of 12.17
:   FEATURE:
:     NAME/KEY: DOMAIN
:     LOCATION: (35)..(153)
:   OTHER INFORMATION: Serum albumin family domain identified by PFam, accession number PR00802A, p-value=3.7e-26, PFam score of 100.3
US-10-273-573-5921

Query Match    100.0%; Score 58; DB 6; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.0002; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Other INFORMATION: Serum albumin family domain identified by PFam, accession US-10-273-573-5921, PFam score of 100.3

Qy      1 AHKSEVYAHRFK 11
Db      33 AHKSEVYAHRFK 43

RESULT 6
US-10-273-573-5924
: Sequence 5924, Application US/10273573
: GENERAL INFORMATION:
:   APPLICANT: Hyseq, Inc
:   FILE REFERENCE: 21272-066
:   CURRENT APPLICATION NUMBER: US/10/273, 573
:   CURRENT FILING DATE: 2002-10-18
:   PRIOR APPLICATION NUMBER: 09/522, 929
:   PRIOR FILING DATE: 2000-04-18
:   PRIOR APPLICATION NUMBER: 09/770, 160
:   NUMBER OF SEQ ID NOS: 10994
:   SOFTWARE: Custom
:   LENGTH: 134
:   TYPE: PRT
:   SEQ ID NO: 5924

```

LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (130)..(154)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00802B, p-value=6.294e-24, raw score of 16.51
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (56)..(185)
; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; US-10-273-573-5924
Query Match 100.0%; Score 58; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.00031; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AHKSEVAHRFK 11
Db 54 AHKSEVAHRFK 64
RESULT 7
US-10-273-573-5923
; Sequence 5923, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273..573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522, 929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770, 160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO: 5923
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (149)..(173)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00802B, p-value=6.294e-24, raw score of 16.51
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (40)..(204)
; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; OTHER INFORMATION: name transport_prot, E-value=1.2e-71, PFam score of 251.5
; US-10-273-573-5923
Query Match 100.0%; Score 58; DB 6; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.00035; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AHKSEVAHRFK 11
Db 38 AHKSEVAHRFK 48
RESULT 8
US-10-273-573-5569
; Sequence 5569, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273..573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522, 929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770, 160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO: 5925
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (161)..(185)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00802B, p-value=6.294e-24, raw score of 16.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (41)..(384)
; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; OTHER INFORMATION: name transport_prot, E-value=2.7e-102, PFam score of 353.3
; US-10-273-573-5925
Query Match 100.0%; Score 58; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.00075; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AHKSEVAHRFK 11
Db 39 AHKSEVAHRFK 49

RESULT 10
US-10-273-573-5926
; Sequence 5926, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, Inc.
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273, 573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522, 929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770, 160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO: 5926
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (158)..(210)
; OTHER INFORMATION: Serum albumin family domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00212, p-value=1.000e-40, raw score of 30.19
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (44)..(503)
; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; OTHER INFORMATION: name transport_prot, E-value=2.6e-126, PFam score of 433.1
US-10-273-573-5926

Query	Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	1 AHKSEVAHRFK 11 1111111111	58	6	550	100.0%	0.0011;	0;	0;	0;	0;
Dy	28 AHKSEVAHRFK 38									

RESULT 12
PCT-US03-18896-26
; Sequence 26, Application PC/TUS0318896
; GENERAL INFORMATION:
; APPLICANT: DYAX Corporation
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052W01
; CURRENT APPLICATION NUMBER: PCT/US03/18896
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388, 642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 26
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-18896-26

Query	Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	1 AHKSEVAHRFK 11 1111111111	58	6	585	100.0%	0.0012;	0;	0;	0;	0;
Dy	2 AHKSEVAHRFK 12									

RESULT 13
PCT-US03-19902-3
; Sequence 3, Application PC/TUS0319902
; GENERAL INFORMATION:
; APPLICANT: DYAX Corporation
; TITLE OF INVENTION: SERUM PROTEIN-ASSOCIATED TARGET-SPECIFIC
; FILE REFERENCE: 10280-052W01
; CURRENT APPLICATION NUMBER: PCT/US03/19902
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/390, 657
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-19902-3

Query	Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	1 AHKSEVAHRFK 11 1111111111	58	6	585	100.0%	0.0012;	0;	0;	0;	0;
Dy	2 AHKSEVAHRFK 12									

RESULT 14
US-10-462-262-26
; Sequence 26, Application US/10462262
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS

Query	Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	1 AHKSEVAHRFK 11 1111111111	58	6	585	100.0%	0.0012;	0;	0;	0;	0;
Dy	2 AHKSEVAHRFK 12									

RESULT 15
US-10-273-573-5927
; Sequence 5927, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, Inc.
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273, 573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522, 929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770, 160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO: 5927
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (188)..(240)
; OTHER INFORMATION: Serum albumin family domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00212, p-value=1.000e-40, raw score of 30.19
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (30)..(534)
; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; OTHER INFORMATION: accession number BL00212, p-value=1.000e-40, raw score of 513.9
; OTHER INFORMATION: name transport_prot, E-value=1.2e-150, PFam score of 513.9
US-10-273-573-5927

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; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIORITY NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 26
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-262-26

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Query Match      100.0%; Score 58; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          1 AHKSEVAHFK 11
           ||||| | | | |
           2 AHKSEVAHFK 12
Db

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RESULT 15

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US-10-602-141-3
; Sequence 3, Application US/10602141
; GENERAL INFORMATION:
; APPLICANT: Salo, Aaron K.
; APPLICANT: Edge, Albert
; TITLE OF INVENTION: SERUM PROTEIN-ASSOCIATED TARGET-SPECIFIC
; TITLE OF INVENTION: LIGANDS AND IDENTIFICATION METHOD THEREFOR
; FILE REFERENCE: 10280-058001
; CURRENT APPLICATION NUMBER: US/10/602,141
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: 2003-06-23
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-602-141-3

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Query Match      100.0%; Score 58; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          1 AHKSEVAHFK 11
           ||||| | | | |
           2 AHKSEVAHFK 12
Db

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Search completed: August 29, 2003, 14:38:01
Job time : 25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:26:35 ; Search time 378 Seconds

(without alignments)
25.328 Million cell updates/sec

Title: US-09-845-726A-1_COPY_2_12
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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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6	58	100.0	11	26	US-10-076-071-4
7	58	100.0	11	27	US-10-186-188-4
8	58	100.0	11	29	US-10-300-664-4
9	58	100.0	12	1	PCT-US00-26952-3
10	58	100.0	12	12	PCT-US00-26952-6
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32	58	100.0	26	23	US-09-846-328A-1
33	58	100.0	26	23	US-09-846-329-1
34	58	100.0	26	23	US-09-846-329A-1
35	58	100.0	54	1	PCT-US01-08656-10524
36	58	100.0	69	30	US-10-424-539-180109
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ALIGNMENTS

RESULT 1
PCT-US00-26952-4
; Sequence 4, Application PC/TUS0026952
; GENERAL INFORMATION
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraj K.R.
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3-PCT
; CURRENT APPLICATION NUMBER: PCT-US00-26952
; CURRENT FILING DATE: 2000-09-30
; EARLIER APPLICATION NUMBER: 60/157,404
; EARLIER FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-26952-4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
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2	58	100.0	11	1	PCT-US02-04275-4	Sequence 4, Appli

Query Match 100.0%; Score 58; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AHKSEVAHRFK 11
 Db 1 AHKSEVAHRFK 11

RESULT 2

PCT-US02-04275-4

; Sequence 4, Application PC/TUS0204275
 ; GENERAL INFORMATION:
 ; APPLICANT: Bar-Or, David
 ; APPLICANT: Lau, Edward
 ; APPLICANT: Curtis, C. Gerald
 ; APPLICANT: Rao, Nagaraja K.R.
 ; APPLICANT: Lau, Edward
 ; APPLICANT: Curtis, C. G.
 ; APPLICANT: Winkler, James V.
 ; APPLICANT: Rao, Nagarao K.R.
 ; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
 ; FILE REFERENCE: 4172-3-2-PCT
 ; CURRENT APPLICATION NUMBER: PCT/US02/04275
 ; CURRENT FILING DATE: 2002-02-13
 ; PRIORITY NUMBER: 09/678,202
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIORITY NUMBER: 60/283,507
 ; PRIOR FILING DATE: 2001-04-11
 ; PRIORITY NUMBER: 09/816,679
 ; PRIOR FILING DATE: 2001-03-22
 ; PRIORITY NUMBER: 60/157,404
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIORITY NUMBER: 60/157,404
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIORITY NUMBER: 60/211,078
 ; PRIOR FILING DATE: 2000-06-13
 ; PRIORITY NUMBER: 60/268,558
 ; PRIOR FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 PCT-US02-04275-4

Query Match 100.0%; Score 58; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
 Db 1 AHKSEVAHRFK 11

Query Match 100.0%; Score 58; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
 Db 1 AHKSEVAHRFK 11

PCT-US02-37136-4

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 Best Local Similarity 100.0%; Pred. No. 0.0068;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AHKSEVAHRFK 11
 Db 1 AHKSEVAHRFK 11

RESULT 4

US-09-578-202A-4

; Sequence 4, Application US/09678202A
 ; GENERAL INFORMATION:
 ; APPLICANT: Bar-Or, David
 ; APPLICANT: Lau, Edward
 ; APPLICANT: Curtis, C. G.
 ; APPLICANT: Rao, Nagarao K.R.
 ; APPLICANT: Winkler, James V.
 ; APPLICANT: Crook, Wannell M.
 ; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
 ; FILE REFERENCE: 4172-3
 ; CURRENT APPLICATION NUMBER: US/09/678,202A
 ; CURRENT FILING DATE: 2000-09-29
 ; PRIORITY NUMBER: 60/157,404
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIORITY NUMBER: 60/211,078
 ; PRIOR FILING DATE: 2000-06-13
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-678-202A-4

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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
 Db 1 AHKSEVAHRFK 11

RESULT 5

US-09-845-726-1

; Sequence 1, Application US/09845726
 ; GENERAL INFORMATION:
 ; APPLICANT: Jackowski, George
 ; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
 ; FILE REFERENCE: 2132-033
 ; CURRENT APPLICATION NUMBER: US/09/845,726
 ; CURRENT FILING DATE: 2001-04-30
 ; NUMBER OF SEQ ID NOS: 1
 ; SEQ ID NO 1
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-845-726-1

Query Match 100.0%; Score 58; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0068;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
 Db 1 AHKSEVAHRFK 11

RESULT 3

PCT-US02-37136-4

; Sequence 4, Application PC/TUS0237136
 ; GENERAL INFORMATION:
 ; APPLICANT: Bar-Or, David
 ; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ORAL CARE
 ; FILE REFERENCE: 4172-75-PCT
 ; CURRENT APPLICATION NUMBER: PCT/US02/37136
 ; CURRENT FILING DATE: 2002-11-19
 ; PRIORITY NUMBER: 60/157,404
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIORITY NUMBER: 60/211,078
 ; PRIOR FILING DATE: 2000-06-13
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

RESULT 6
 US-10-076-071-4
 ; Sequence 4, Application US/10076071
 ; GENERAL INFORMATION:
 ; APPLICANT: Bar-Or, David
 ; APPLICANT: Curtis, C. Gerald
 ; APPLICANT: Lau, Edward
 ; APPLICANT: Rao, Nagarao K.R.
 ; APPLICANT: Winkler, James V.
 ; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
 ; FILE REFERENCE: 4172-3-2
 ; CURRENT FILING DATE: 2002-02-13
 ; PRIOR APPLICATION NUMBER: 09/678,202
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: US/10/076,071
 ; PRIOR FILING DATE: 2002-02-13
 ; SEQ ID NO 4
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-076-071-4

Query Match 100.0%; Score 58; DB 27; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00068; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
 Db 1 AHKSEVAHRFK 11

RESULT 8
 US-10-300-664-4
 ; Sequence 4, Application US/10300664
 ; GENERAL INFORMATION:
 ; APPLICANT: Bar-Or, David
 ; APPLICANT: Curtis, C. G.
 ; APPLICANT: Lau, Edward
 ; APPLICANT: Rao, Nagarao K.R.
 ; APPLICANT: Winkler, James V.
 ; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
 ; FILE REFERENCE: 4172-3
 ; CURRENT APPLICATION NUMBER: US/10/300,664
 ; CURRENT FILING DATE: 2002-11-19
 ; PRIOR APPLICATION NUMBER: US/10/300,664
 ; PRIOR FILING DATE: 2002-11-19
 ; PRIOR APPLICATION NUMBER: 60/157,404
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,404
 ; PRIOR FILING DATE: 1999-10-01
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 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,404
 ; PRIOR FILING DATE: 1999-10-01
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-300-664-4

Query Match 100.0%; Score 58; DB 29; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00068; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
 Db 1 AHKSEVAHRFK 11

RESULT 7
 US-10-186-168-4
 ; Sequence 4, Application US/10186168
 ; GENERAL INFORMATION:
 ; APPLICANT: Bar-Or, David
 ; APPLICANT: Curtis, C. G.
 ; APPLICANT: Lau, Edward
 ; APPLICANT: Rao, Nagarao K.R.
 ; APPLICANT: Winkler, James V.
 ; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
 ; FILE REFERENCE: 4172-3-4
 ; CURRENT FILING DATE: 2002-06-27
 ; PRIOR APPLICATION NUMBER: US/09/678,202
 ; PRIOR APPLICATION NUMBER: 60/157,404
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR FILING DATE: 2000-06-13
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-186-168-4

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RESULT 10
PCT-US00-26952-6
; Sequence 6, Application PC/TUS0026952
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3-2-PCT
; CURRENT APPLICATION NUMBER: PCT/TUS00/26952
; CURRENT FILING DATE: 2000-09-30
; EARLIER APPLICATION NUMBER: 60/157,404
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 60/211,078
; EARLIER FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:variant
PCT-US00-26952-6

Query Match 100.0%; Score 58; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00075; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
Db 2 AHKSEVAHREFK 12

RESULT 12
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; Sequence 6, Application PC/TUS0204275
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. Gerald
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
; FILE REFERENCE: 4172-3-2-PCT
; CURRENT APPLICATION NUMBER: PCT/TUS02/04275
; CURRENT FILING DATE: 2002-02-13
; PRIORITY APPLICATION NUMBER: 09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIORITY APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIORITY APPLICATION NUMBER: 09/816,679
; PRIOR FILING DATE: 2001-03-22
; PRIORITY APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIORITY APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIORITY APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; PRIORITY APPLICATION NUMBER: 60/268,558
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO: 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1) ; (1)
; OTHER INFORMATION: ACETYLATION
PCT-US02-04275-6

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Qy 1 AHKSEVAHREFK 11
Db 2 AHKSEVAHREFK 12

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; Sequence 3, Application PC/TUS0237136
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David

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; FILE REFERENCE: 4172-75-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/37136
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-37136-3

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Db      2 AHKSEVAHREFK 12
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RESULT 14
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; Sequence 6, Application PC/TUS0237136
; GENERAL INFORMATION:
; APPLICANT: Bar-On, David
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ORAL CARE
; FILE REFERENCE: 4172-75-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/37136
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
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RESULT 15
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; Sequence 3, Application US/09678202A
; GENERAL INFORMATION:
; APPLICANT: Bar-On, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarao K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/09/678,202A
; CURRENT FILING DATE: 2000-09-29

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; PRIOR APPLICATION NUMBER: 60/157,404
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; PRIOR APPLICATION NUMBER: 60/211,078
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; ORGANISM: Homo sapiens
US-09-678-202A-3

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2003, 14:28:50 ; Search time 56 Seconds

(without alignments)
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Title: US-09-845-726a-1_COPY_2_12

Perfect score: 58

Sequence: 1 AHKSEVAHREFK 11

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
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2	58	100.0	11	12	US-10-300-664-3	Sequence 2, Appli
3	58	100.0	11	15	US-10-076-071-4	Sequence 3, Appli
4	58	100.0	11	16	US-10-186-168-4	Sequence 4, Appli
5	58	100.0	12	11	US-09-846-347-1	Sequence 5, Appli
6	58	100.0	12	12	US-10-300-664-3	Sequence 6, Appli
7	58	100.0	12	12	US-10-300-664-6	Sequence 7, Appli
8	58	100.0	12	15	US-10-076-071-3	Sequence 8, Appli
9	58	100.0	12	15	US-10-186-071-6	Sequence 9, Appli
10	58	100.0	12	16	US-10-186-168-3	Sequence 10, Appli
11	58	100.0	12	16	US-10-186-168-6	Sequence 11, Appli
12	58	100.0	13	10	US-09-845-764-1	Sequence 12, Appli
13	58	100.0	17	10	US-09-845-727-1	Sequence 13, Appli
14	58	100.0	24	10	US-09-846-328-1	Sequence 14, Appli
15	58	100.0	26	10	US-09-846-329-1	Sequence 15, Appli

16	58	100.0	14	14	US-10-074-956-24	Sequence 24, Appli
17	58	100.0	241	14	US-10-074-956-27	Sequence 25, Appli
18	58	100.0	268	14	US-10-074-956-28	Sequence 26, Appli
19	58	100.0	585	10	US-09-929-552-2	Sequence 27, Appli
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21	58	100.0	585	11	US-09-984-010-26	Sequence 29, Appli
22	58	100.0	585	11	US-09-833-041-18	Sequence 30, Appli
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25	58	100.0	604	11	US-09-984-010-7	Sequence 33, Appli
26	58	100.0	609	11	US-09-919-03-370	Sequence 34, Appli
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29	58	100.0	610	15	US-10-237-186-2	Sequence 37, Appli
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36	58	100.0	651	14	US-10-153-604-133	Sequence 44, Appli
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39	58	100.0	652	12	US-10-153-604-105	Sequence 47, Appli
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44	58	100.0	652	14	US-10-153-064-132	Sequence 52, Appli
45	58	100.0	653	12	US-10-153-604-131	Sequence 53, Appli

ALIGNMENTS

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 ; Sequence 1, Application US/09845726
 ; Applicant: JACKOWSKI, George
 ; Patent No. US20020160417A1
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
 ; TITLE OF INVENTION: OF 1424 DALTONS
 ; CURRENT APPLICATION NUMBER: US/09/845,726
 ; CURRENT FILING DATE: 2001-04-30
 ; NUMBER OF SEQ ID NOs: 1
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-845-726-1

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QY 1 AHKSEVAHREFK 11
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RESULT 2
 US-10-300-664-4
 ; Sequence 4, Application US/10300664
 ; Publication No. US2003015811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bar-Or, David
 ; APPLICANT: Curtiss, C. G.
 ; APPLICANT: Lau, Edward
 ; APPLICANT: Rao, Nagaraju K.R.
 ; APPLICANT: Winkler, James V.

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RESULT 4
US-10-186-168-4
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/300, 664
; PRIORITY NUMBER: US/09/678, 202
; CURRENT FILING DATE: 2002-11-19
; PRIORITY FILING DATE: 2000-09-19
; PRIORITY APPLICATION NUMBER: US/09/678, 202
; PRIORITY APPLICATION NUMBER: US/09/678, 202
; PRIORITY APPLICATION NUMBER: 60/157, 404
; PRIORITY FILING DATE: 1999-10-01
; PRIORITY APPLICATION NUMBER: 60/211, 078
; PRIORITY FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT ; ORGANISM: Homo sapiens
US-10-300-664-4

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; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
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; CURRENT APPLICATION NUMBER: US/10/076, 071
; Sequence 4, Application US/100766071
; Publication No. US20030060408A1
; GENERAL INFORMATION:
; PRIORITY NUMBER: US/09/678, 202
; PRIORITY FILING DATE: 2000-09-19
; PRIORITY APPLICATION NUMBER: 60/289, 507
; PRIORITY FILING DATE: 2001-04-11
; PRIORITY APPLICATION NUMBER: 09/816, 679
; PRIORITY FILING DATE: 2001-03-12
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; PRIORITY FILING DATE: 2000-06-13
; PRIORITY APPLICATION NUMBER: 60/268, 558
; PRIORITY FILING DATE: 2001-02-13
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US-10-076-071-4

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; Publication No. US2003015811A1
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; PRIORITY FILING DATE: 1999-10-01
; PRIORITY APPLICATION NUMBER: 60/211, 078
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; TYPE: PRT ; ORGANISM: Homo sapiens
US-10-300-664-3

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PRIOR FILING DATE: 2000-06-13
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; PRIOR FILING DATE: 2001-02-13
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; SOFTWARE: PatentIn version 3.0
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; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1).(1)
; OTHER INFORMATION: ACETYLATION
US-10-076-071-6

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Db 2 AHKSEVAHRFK 12

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; Publication No. US20030130185A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarjao K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/186,168
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-39
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
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; LENGTH: 12
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; ORGANISM: Homo sapiens
US-10-186-168-3

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Db 2 AHKSEVAHRFK 12

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; Publication No. US20030130185A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarjao K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.

;

;

TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/186,168
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-39
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
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; ORGANISM: Homo sapiens
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; Patent No. US20020160938A1
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; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; FILE REFERENCE: 2132-037
; CURRENT APPLICATION NUMBER: US/09/845,764
; CURRENT FILING DATE: 2001-04-30
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; Patent No. US2002016018A1
; GENERAL INFORMATION:
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; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
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; CURRENT APPLICATION NUMBER: US/09/845,727
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; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
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US-09-845-727-1

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; Patent No. US20020160531A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 2753 DALTONS
; FILE REFERENCE: 2132_051
; CURRENT APPLICATION NUMBER: US/09/846,328
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.1
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; TYPE: PRT
; ORGANISM: Homo sapiens
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RESULT 15

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; Patent No. US2002016117A1
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; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having A Molecular
; TITLE OF INVENTION: OF 2937 Dalton
; FILE REFERENCE: 2132_052
; CURRENT APPLICATION NUMBER: US/09/846,329
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.1
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; ORGANISM: Homo sapiens
US-09-846-329-1

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Db      2 AHKSEVAHRFK 12

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Post-processing: Minimum Match 0%

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2: /cn2_6/ptodata/1/iaa/5B_COMBO.pep:*

3: /cn2_6/ptodata/1/iaa/6A_COMBO.pep:*

4: /cn2_6/ptodata/1/iaa/6B_COMBO.pep:*

5: /cn2_6/ptodata/1/iaa/PCITS_COMBO.pep:*

6: /cn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	13	2 US-08-803-364-7	Sequence 7, Appli
2	58	100.0	13	2 US-09-024-198-13	Sequence 13, Appli
3	58	100.0	13	1 US-09-186-409-13	Sequence 1, Appli
4	58	100.0	585	1 US-08-153-799-14	Sequence 14, Appli
5	58	100.0	585	1 US-08-448-196A-3	Sequence 3, Appli
6	58	100.0	585	2 US-08-702-572-2	Sequence 2, Appli
7	58	100.0	585	3 US-08-769-746-2	Sequence 2, Appli
8	58	100.0	609	1 US-08-222-619-3	Sequence 4, Appli
9	58	100.0	609	1 US-08-433-037-4	Sequence 4, Appli
10	58	100.0	609	4 US-08-897-956A-2	Sequence 2, Appli
11	58	100.0	609	5 PCT-US97-04075-3	Sequence 7, Appli
12	58	100.0	610	2 US-08-797-689-2	Sequence 2, Appli
13	53	91.4	783	1 US-08-256-938-2	Sequence 2, Appli
14	58	100.0	787	2 US-08-797-689-16	Sequence 4, Appli
15	58	100.0	787	2 US-08-997-956A-3	Sequence 16, Appli
16	58	100.0	978	4 US-08-897-956A-3	Sequence 3, Appli
17	58	98.3	584	1 US-08-448-196A-7	Sequence 1, Appli
18	57	98.3	582	1 US-08-134-638-1	Sequence 4, Appli
19	53	91.4	583	1 US-08-448-196A-4	Sequence 6, Appli
20	53	91.4	86.2	13 2 US-09-024-198-12	Sequence 12, Appli
21	50	86.2	13 2 US-09-024-198-12	Sequence 12, Appli	
22	50	86.2	13 2 US-09-086-409-12	Sequence 12, Appli	
23	50	86.2	16 2 US-08-803-364-1	Sequence 10, Appli	
24	50	86.2	16 2 US-09-024-198-10	Sequence 10, Appli	
25	50	86.2	16 2 US-09-186-409-10	Sequence 5, Appli	
26	50	82.8	583	1 US-08-448-196A-5	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-803-364-7
; Sequence 7, Application US/08803364
; Patent No. 5864044
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803-364
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/_____,
; FILING DATE: 20 FEB 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: A-6888
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: NO
; US-08-803-364-7

Query Match Score 58 ; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.0e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AHKSEVAHRK 11
|||||||

Db 1 AHKSEVAHRFK 11

RESULT 2
US-09-024-198-13
; Sequence 13, Application US/09024198
; Patent No. 5912323
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULIA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,198
; FILING DATE: 17 FEB 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/024,198
; FILING DATE: 17 FEB 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/024,198
; FILING DATE: 17 FEB 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REFERENCE/DOCKET NUMBER: A-6988
; TELECOMMUNICATION INFORMATION:
; NAME: KIT, Gordon
; REFERENCE/DOCKET NUMBER: A-6988
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7060
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO

US-09-024-198-13
; Sequence 13, Application US/09024198
; Patent No. 5948629
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULIA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-186-409-13
; Sequence 13, Application US/09186409
; Patent No. 5948629
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULIA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,799
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07-847975
; FILING DATE: 06-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8909916.2
; FILING DATE: 29-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00650

RESULT 3
US-09-186-409-13
; Sequence 13, Application US/09186409
; Patent No. 5948629
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULIA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07-847975
; FILING DATE: 06-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8909916.2
; FILING DATE: 29-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00650

FILING DATE: 26-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/775952
; FILING DATE: 29-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R Hain
; REGISTRATION NUMBER: 24864
; REFERENCE/DOCKET NUMBER: 92H832
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 665 2400
; TELEX: (908) 771 6159
; FAX: 219484
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Region
; LOCATION: 369..419
; OTHER INFORMATION: /note= "Alternative C-termini of
; HSA(1-n)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..585
; OTHER INFORMATION: /note= "Amino acid sequence of
; natural HSA"
; OTHER INFORMATION: natural HSA

US-08-153-799-14

Query Match Score 58; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
Db 2 AHKSEVAHREFK 12

RESULT 5
US-08-448-196A-3
; Sequence 3, Application US/08448196A
; Patent No. 5780594
; GENERAL INFORMATION:
; APPLICANT: CARTER, DANIEL C.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
; TITLE OF INVENTION: RELATED PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NASA
; STREET: MARSHALL SPACE FLIGHT CENTER
; CITY: HUNTSVILLE
; STATE: ALABAMA
; COUNTRY: USA
; ZIP: 35812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448-196A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BROAD JR., ROBERT L.
; REGISTRATION NUMBER: 18,757
; REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
; TELECOMMUNICATION INFORMATION:

US-08-448-196A-3

Query Match Score 58; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
Db 2 AHKSEVAHREFK 12

RESULT 6
US-08-984-176-1
; Sequence 1, Application US/08984176
; Patent No. 5948669
; GENERAL INFORMATION:
; APPLICANT: CARTER, DANIEL C.
; APPLICANT: HO, JOSEPH X
; APPLICANT: RUKEV, FLORIAN
; TITLE OF INVENTION: OXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT
; TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER
; FILE REFERENCE: 08/984-176
; CURRENT APPLICATION NUMBER: US/08/984-176
; CURRENT FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-984-176-1

Query Match Score 58; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
Db 2 AHKSEVAHREFK 12

RESULT 7
US-08-702-572-2
; Sequence 2, Application US/08702572
; Patent No. 5965386
; GENERAL INFORMATION:
; APPLICANT: Kerry-Williams, Sean M
; APPLICANT: Gilbert, Sarah C
; TITLE OF INVENTION: Yeast Strains and Modified Albumins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Centeon L.L.C.
; STREET: 1020 First Avenue
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448-196A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BROAD JR., ROBERT L.
; REGISTRATION NUMBER: 18,757
; REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
; TELECOMMUNICATION INFORMATION:

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,572
; FILING DATE: 11-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/23857
; FILING DATE: 1-MAR-1995
; APPLICATION NUMBER: GB 9404270.2
; FILING DATE: 5-MAR-1994

ATTORNEY/AGENT INFORMATION:
; NAME: Naomi Biswas
; REGISTRATION NUMBER: 38,384
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610/878/4234
; TELEFAX: 610/878/4221
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-702-572-2

Query Match 100.0%; Score 58; DB 3; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12

RESULT 9
US-08-222-619-3
; Sequence 3, Application US/08222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afanin: A Human Serum Albumin-Like
; TITLE OF INVENTION: protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

US-08-222-619-3

Query Match 100.0%; Score 58; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0042; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
Db 26 AHKSEVAHRFK 36

RESULT 10
US-08-433-037-4
; Sequence 4, Application US/08433037
; Patent No. 5707828
; GENERAL INFORMATION:
; APPLICANT: Sreekrishna, Kotikanyadan
; APPLICANT: Barr, Kathryn A.
; APPLICANT: Brierley, Russell A.
; APPLICANT: Thill, Gregory P.
; APPLICANT: Tschopp, Juerg F.
; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
; TITLE OF INVENTION: PICTIA PASTORIS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York

US-08-769-746-2

Query Match 100.0%; Score 58; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0042; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
Db 26 AHKSEVAHRFK 36

RESULT 8
US-08-769-746-2
; Sequence 2, Application US/08769746
; Patent No. 6274305
; GENERAL INFORMATION:
; APPLICANT: Sonnenschein, Carlos
; TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,746
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cattil, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: MBRI-02584
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-769-746-2

; COUNTRY: U.S.A.
 ; ZIP: 11530-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/433,037
 ; FILING DATE: 03-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DIGI9110, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 91082
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 723-3666
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 609 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-433-037-4

Query Match 100.0%; Score 58; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.0042;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AHKSEVAHRFK	11
	1111111111		
Db	26	AHKSEVAHRFK	36

RESULT 11
 US-08-897-956A-2
 ; Sequence 2, Application US/08897956A
 ; GENERAL INFORMATION:
 ; APPLICANT: Mary Ellen Digan
 ; APPLICANT: Phillip Lake
 ; APPLICANT: Hermann Gram
 ; TITLE OF INVENTION: Fusion Polypeptides
 ; FILE REFERENCE: 600-724/CPA
 ; CURRENT APPLICATION NUMBER: US/08/897,956A
 ; CURRENT FILING DATE: 1997-07-21
 ; PRIOR APPLICATION NUMBER: 60/022,689
 ; PRIOR FILING DATE: 1996-07-26
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 609
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-08-897-956A-2

Query Match 100.0%; Score 58; DB 4; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.0042;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AHKSEVAHRFK	11
	1111111111		
Db	26	AHKSEVAHRFK	36

RESULT 12
 PCT-US95-04075-3
 ; Sequence 3, Application PC/TU9504075
 ; GENERAL INFORMATION:
 ; APPLICANT: AMGEN INC.
 ; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like

; TITLE OF INVENTION: protein
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Center, Patent Operations/RRC
 ; STREET: 1840 DeHavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: U.S.
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/04075
 ; FILING DATE:
 ; CLASSIFICATION:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 609 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; PCT-US95-04075-3

Query Match 100.0%; Score 58; DB 5; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.0042;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AHKSEVAHRFK	11
	1111111111		
Db	26	AHKSEVAHRFK	36

RESULT 13
 US-08-797-689-2
 ; Sequence 2, Application US/08797689
 ; Patent No. 587969
 ; GENERAL INFORMATION:
 ; APPLICANT: Fleer, Reinhard
 ; APPLICANT: Fournier, Alain
 ; APPLICANT: Guittot, Jean-Dominique
 ; APPLICANT: Jung, Gerard
 ; APPLICANT: Yeh, Patrice
 ; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
 ; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
 ; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.1
 ; SOFTWARE: Word 5.1 (PatentIn)
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 31-JAN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/797,689
 ; FILING DATE: 28-JUL-1994
 ; APPLICATION NUMBER: US 08/256,927
 ; FILING DATE: 31-JAN-1992
 ; APPLICATION NUMBER: FR 92/01064
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/FR93/00085

; FILING DATE: 28-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith Ph.D., Julie K.
 ; REGISTRATION NUMBER: P-38,619
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3839
 ; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 610 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Protein
 ; US-08-737-689-2

Query Match 100.0%; Score 58; DB 2; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0.0042;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AHKSEVAHRFK 11
Db	26 AHKSEVAHRFK 36

RESULT 14
 US-08-256-938-2
 ; Sequence 2, Application US/03256938
 ; Patent No. 5665863

; GENERAL INFORMATION:
 ; APPLICANT: Yeh, Patrice
 ; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
 ; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
 ; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.1
 ; SOFTWARE: Word 5.0 (PatentIn)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/256,938

; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 92/01065
 ; FILING DATE: 31-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goodman, Rosanne
 ; REGISTRATION NUMBER: 32,534
 ; REFERENCE/DOCKET NUMBER: ST92007-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3817
 ; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 787 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-256-938-4

Query Match 100.0%; Score 58; DB 1; Length 787;
 Best Local Similarity 100.0%; Pred. No. 0.0056;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
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 Db 204 AHKSEVAHRFK 214

Search completed: August 29, 2003, 14:30:04
 Job time : 30 secs

; FILING DATE: 28-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith Ph.D., Julie K.
 ; REGISTRATION NUMBER: P-38,619
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3817
 ; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 783 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-256-938-2

Query Match 100.0%; Score 58; DB 1; Length 783;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw mode1

Run on: August 29, 2003, 14:13:44 ; Search time 82 Seconds

(without alignments)
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 Perfect score: 58

Sequence: 1 AHKSEVAHREFK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	58	100.0	11	22	AAB74358	Reactive oxygen sp
2	58	100.0	11	23	AAE14802	Human reactive oxy
3	58	100.0	11	24	ABG75656	Congestive heart f
4	58	100.0	12	22	AAB74357	Reactive oxygen sp
5	58	100.0	12	22	AAB74370	Human reactive oxy
6	58	100.0	12	23	AAE14801	Blopolymer marker
7	58	100.0	12	23	AAE14804	Human reactive oxy
8	58	100.0	12	24	ABP99709	Crook WM;
9	58	100.0	13	19	AAM74538	Human serum albumi

102 (a)

ALIGNMENTS

RESULT 1	AAB74368	ID	AAB74368 standard; peptide; 11 AA.
XX	XX	XX	XX
		AC	AAB74368;
		XX	XX
		DT	02-JUL-2001 (first entry)
		XX	XX
		DE	Reactive oxygen species inhibitory peptide #4.
		XX	KW
		XX	ROS: reactive oxygen species; metal binding; ischemia;
		OS	Synthetic.
		XX	KW
		PD	neurodegenerative.
		XX	KW
		PR	WO200125365-A1.
		XX	XX
		PD	12-APR-2001.
		XX	XX
		PR	13-JUN-2000; 2000US-0211078.
		XX	XX
		PR	01-OCT-1999; 99US-0157404.
		XX	XX
		PR	29-SEP-2000; 2000WO-US26952.
		XX	XX
		PR	01-OCT-1999; 99US-0157404.
		XX	XX
		PR	13-JUN-2000; 2000US-0211078.
		XX	XX
		PA	(BARO/) BAR-OR D.
		PA	(CURT/) CURTIS C. G.
		PA	(LAUE/) LAU E.
		PA	(RAON/) RAO N K R.
		PA	(WINK/) WINKLER J. V.
		PA	(CROOK/) CROOK W. M.
		XX	Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;

XX WPI; 2001-328322/34.
 DR
 XX

PT Metal binding peptide compounds prevent damage by reactive oxygen species in animal organs and tissues, useful for reperfusing an ischemic tissue or organ with cerebral or cardiovascular disease -
 PR transplantation and treating e.g. ischemia, neurological and cardiovascular diseases -
 XX

PS Example 10; Page 43; 124pp; English.

XX The present invention relates to metal binding peptides that prevent damage by reactive oxygen. The peptides may be used for reperfusing an ischemic tissue or organ with cerebral or cardiovascular disease, for treating neurological trauma and for neurodegenerative disease. The present sequence is a reactive oxygen species inhibitory peptide.

XX Sequence 11 AA;
 SQ

Query Match 100.0%; Score 58; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.2e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AHKSEVAHRFK 11
 ||||| |||||
 Db 1 AHKSEVAHRFK 11
 ||||| |||||

DR 24-FEB-2003 (first entry)

DT XX

DE Human reactive oxygen species generation inhibiting peptide #2.
 XX Reactive oxygen species; ROS; metal binding peptide; angiogenesis; embryo implantation; endometriosis; tumour; hypertrophy; psoriasis;
 KW connective tissue disorder; ocular angiogenic disease; polyposis;
 KW cardiovascular disease; cerebral vascular disease; immune disorder;
 KW sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease;
 KW cancer; cystic fibrosis; diabetes; hepatitis C; infertility;
 KW inflammation; inflammatory bowel disease; neurological disease;
 KW multiple sclerosis; pancreatitis; human.

XX Homo sapiens.

XX WO200264620-A2.

XX PD 22-AUG-2002.

XX PF 13-FEB-2002; 2002WO-US04275.

XX XX 13-FEB-2001; 2001US-268558P.

PR 22-MAR-2001; 2001US-0816679.

PR 04 APR 2001; 2001US-281648P.

PR 11-APR-2001; 2001US-283507P.

XX (DMIB-) DMI BIOSCIENCES INC.

XX PI Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;

XX DR WPI; 2002-691590/74.

XX New method for the inhibition of angiogenesis and the treatment of angiogenic disease, sepsis, and a disease involving acidosis, comprises the administration of a specified peptide or its salt -

XX PS Example 10; Page 56; 129pp; English.

XX CC The invention relates to a method for reducing molecular, cellular and tissue damage done by reactive oxygen species (ROS) and also

reducing concentration of a metal ion in an animal using specific metal-binding peptides and their derivatives that bind metal ions. The compounds of the invention are useful for inhibiting angiogenesis (including required for embryo implantation e.g. in endometriosis), and for treating angiogenic diseases, such as tumour (preferably a benign tumour), tumour metastasis, hypertension, connective tissue disorder, psoriasis, ocular angiogenic disease, cardiovascular disease, cerebral vascular disease, polyposis, obesity, immune disorder, sepsis, and a disease or condition involving acidosis. The compounds are also useful in the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension, senility and impotence), arthritis, asthma, autoimmune diseases, cancer, chronic granulomatous disease, cirrhosis, colitis, Crohn's disease, cystic fibrosis, (neuro)degenerative diseases, diabetes (diabetic retinopathy), renal disease, impotence and peripheral vascular disease, eye diseases, emphysema, head and traumatic brain injury, hepatitis C, infertility, inflammatory bowel disease, neoplastic diseases, metastasis, ischaemia, neoplastic disease, peripheral vascular disease, prion disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock, tissue damage, toxic reactions (e.g. poisoning (herbicide, transition metal, carbon monoxide, and antibiotic toxicity). The present sequence is a human peptide that inhibits generation of reactive oxygen species (ROS).

SQ Sequence 11 AA;
 Query Match 100.0%; Score 58; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.2e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
 ||||| |||||
 Db 1 AHKSEVAHRFK 11
 ||||| |||||

RESULT 3
 ABG7556
 ID ABG7556 standard; Peptide; 11 AA.
 XX AC ABG7556;
 XX DT 13-MAY-2003 (first entry)
 DE XX Congestive heart failure disease specific marker #1.
 XX KW Biopolymer marker; serum albumin; disease specific marker; congestive heart failure.

XX XX Unidentified.

OS XX US2002160417-A1.

OS XX Unidentified.

OS XX US2002160417-A1.

OS XX Unidentified.

Self.

XX DR WPI; 2003-246641/25.

XX PT Novel biopolymer marker such as serum albumin having specific molecular weight, useful in indicating disease state such as congestive heart failure -

PT PT

PT PT

PT PT

PT PT

PT PT

XX PS Claim 1; Page 7; 10pp; English.
 XX CC The invention relates to a biopolymer marker such as serum albumin having
 CC a molecular weight of about 142 daltons, useful in indicating at least
 CC one particular disease state. The biopolymer marker is useful for
 CC indicating at least one particular disease state such as congestive heart
 CC failure and an antigen in immunoassays for the detection of those
 CC individuals suffering from the disease known to be evidenced by the
 CC marker sequence. The biopolymer marker rapidly and accurately diagnoses a
 CC disease state such as congestive heart failure and allows physicians to
 CC identify asymptomatic patients before they develop the disease state.
 CC This sequence represents a congestive heart failure disease specific
 CC marker.

XX SQ Sequence 11 AA;
 XX Query Match 100.0%; Score 58; DB 24; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.2e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AHKSEVAHRFK 11
 Db 111111111111111111
 1 AHKSEVAHRFK 11
 1 AHKSEVAHRFK 11

RESULT 4
 ID AAB74367 standard; peptide; 12 AA.
 XX AC AAB74367;
 XX DT 02-JUL-2001 (first entry)
 XX DE Reactive oxygen species inhibitory peptide #3.
 XX KW ROS; reactive oxygen species; metal binding; ischemia;
 KW neurodegenerative.
 XX OS Synthetic.
 XX PI Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;
 XX DR WPT; 2001-328322/34.
 XX PT Metal binding peptide compounds prevent damage by reactive oxygen
 PT species in animal organs and tissues, useful for reperfusion,
 PT transplantation and treating e.g. ischemia, neurological and
 PT cardiovascular diseases -
 XX PS Example 10; Page 43; 124pp; English.
 XX CC The present invention relates to metal binding peptides that prevent
 CC damage by reactive oxygen. The peptides may be used for reperfusing
 CC an ischemic tissue or organ with cerebral or cardiovascular ischemia,
 CC for treating neurological trauma and for neurodegenerative disease.
 XX CC The present sequence is a reactive oxygen species inhibitory peptide.

XX SQ Sequence 12 AA;
 XX Query Match 100.0%; Score 58; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AHKSEVAHRFK 11
 111111111111111111
 Db 2 AHKSEVAHRFK 12
 2 AHKSEVAHRFK 12

XX PS The present invention relates to metal binding peptides that prevent
 PT damage by reactive oxygen. The peptides may be used for reperfusing
 PT an ischemic tissue or organ with cerebral or cardiovascular ischemia,
 CC for treating neurological trauma and for neurodegenerative disease.
 CC The present sequence is a reactive oxygen species inhibitory peptide.

RESULT 6
 AAE14801

ID	AAE14801 standard; peptide; 12 AA.	Qy	1 AHKSEVAHRFK 11 1 1
XX		Db	2 AHKSEVAHRFK 12
AC	AAE14801;		
XX			
DT	24-FEB-2003 (first entry)		
DE	Human reactive oxygen species generation inhibiting peptide #1.		
XX		RESULT 7	
KW	Reactive oxygen species; ROS; metal-binding peptide; angiogenesis;	AAE14804	
KW	embryo implantation; endometriosis; tumour; hypertrophy; psoriasis;	ID AAE14804 standard; Peptide; 12 AA.	
KW	connective tissue disorder; ocular angiogenic disease; polyposis;	XX	
KW	cardiovascular disease; cerebral vascular disease; immune disorder;	AC	
KW	sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease;	AAE14804;	
KW	cancer; cystic fibrosis; diabetes; hepatitis C; infertility;	XX	
KW	inflammation; inflammatory bowel disease; neurological disease;	DT	24-FEB-2003 (first entry)
KW	multiple sclerosis; pancreatitis; human.	XX	
XX	Homo sapiens.	DE	Human reactive oxygen species generation inhibiting peptide #4.
OS		XX	
XX		KW	Reactive oxygen species; ROS; metal-binding peptide; angiogenesis;
PN	WO200264620-A2.	KW	embryo implantation; endometriosis; tumour; hypertrophy; psoriasis;
XX		KW	connective tissue disorder; ocular angiogenic disease; polyposis;
PD	22-AUG-2002.	KW	cardiovascular disease; cerebral vascular disease; immune disorder;
XX		KW	sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease;
PF	13-FEB-2002; 2002WO-US04275.	KW	cancer; cystic fibrosis; diabetes; hepatitis C; infertility;
XX		KW	inflammation; inflammatory bowel disease; neurological disease;
PR	13-FEB-2001; 2001US-268558P.	XX	multiple sclerosis; pancreatitis; human.
PR	22-MAR-2001; 2001US-0816679.	OS	
PR	04-APR-2001; 2001US-281648P.	OS	
PR	11-APR-2001; 2001US-283507P.	Synthetic.	
XX	(DMIB-) DMI BIOSCIENCES INC.		
PA		XX	
XX	Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;	Key	Location/Qualifiers
PI		FT	1 /note= "N-terminal acetylated"
XX	DR WPI; 2002-691590/74.	FT	
XX		XX	
PT	New method for the inhibition of angiogenesis and the treatment of	PR	22-AUG-2002.
PT	angiogenic disease, sepsis, and a disease involving acidosis, comprises	XX	13-FEB-2002; 2002WO-US04275.
PT	the administration of a specified peptide or its salt -	XX	13-FEB-2001; 2001US-268558P.
XX		PR	13-MAR-2001; 2001US-0816679.
PS	Example 10; Page 56; 129pp; English.	PR	04-APR-2001; 2001US-281648P.
XX		PR	11-APR-2001; 2001US-283507P.
CC	The invention relates to a method for reducing molecular, cellular	XX	XX
CC	and tissue damage done by reactive oxygen species (ROS) and also	PA	(DMIB-) DMI BIOSCIENCES INC.
CC	reducing concentration of a metal ion in an animal using specific	XX	
CC	metal binding peptides and their derivatives that bind metal ions.	PI	Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;
CC	The compounds of the invention are useful for inhibiting angiogenesis	XX	XX
CC	(including required for embryo implantation e.g. in endometriosis), and	DR	WPI; 2002-691590/74.
CC	for treating angiogenic diseases, such as tumour (preferably a benign	XX	
CC	tumour), tumour metastasis, hypertrophy, connective tissue disorder,	PT	New method for the inhibition of angiogenesis and the treatment of
CC	psoriasis, ocular angiogenic disease, cardiovascular disease, prion	PT	angiogenic disease, sepsis, and a disease involving acidosis, comprises
CC	vascular disease, polyposis, obesity, immune disorder, sepsis, and a	PT	the administration of a specified peptide or its salt -
CC	disease or condition involving acidosis. The compounds are also useful in	XX	
CC	the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension,	XX	Example 10; Page 57; 129pp; English.
CC	senility and impotence), arthritis, asthma, autoimmune diseases,	XX	
CC	cancer, chronic granulomatous disease, cirrhosis, colitis, Crohn's	CC	The invention relates to a method for reducing molecular, cellular
CC	disease, cystic fibrosis, (neuro)degenerative diseases, diabetes	CC	and tissue damage done by reactive oxygen species (ROS), and also
CC	(diabetic retinopathy), renal disease, impotence and peripheral vascular	CC	reducing concentration of a metal ion in an animal using specific
CC	disease), eye diseases, emphysema, head and traumatic brain injury,	CC	metal-binding peptides and their derivatives that bind metal ions.
CC	hepatitis C, infertility, inflammation, inflammatory bowel disease,	CC	The compounds of the invention are useful for inhibiting angiogenesis
CC	metastasis, ischaemia, neoplastic diseases, neurological diseases,	CC	(including required for embryo implantation e.g. in endometriosis), and
CC	multiple sclerosis, pancreatitis, peripheral vascular disease, prion	CC	for treating angiogenic diseases, such as tumour (preferably a benign
CC	disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock,	CC	tumour, metastasis, hypertrophy, connective tissue disorder,
CC	tissue damage, toxic reactions (e.g. poisonings (herbicide, metal, carbon monoxide, and antibiotic toxicity). The present	CC	psoriasis, ocular angiogenic disease, cardiovascular disease, cerebral
CC	sequence is a human peptide that inhibits generation of reactive	CC	vascular disease, polyposis, obesity, immune disorder, sepsis, and a
CC	oxygen species (ROS).	CC	disease or condition involving acidosis. The compounds are also useful in
XX	Sequence 12 AA;	CC	the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension,
SQ		CC	senility and impotence), arthritis, asthma, autoimmune diseases,
Query Match	100.0%	DB	Crohn's, colitis, Crohn's
Best Local Similarity	100.0%	Length	CC
Matches	0;	Pred. No.	CC
11; Conservative	0;	Mismatches	CC
		Indels	CC
		Gaps	CC
		0;	CC

CC metastasis, ischaemia, neoplastic diseases, neurological diseases,
 CC multiple sclerosis, pancreatitis, peripheral vascular disease, prion
 CC disease, pulmonary embolism, reperfusion, scleroedema, sepsis, shock,
 CC tissue damage, toxic reactions (e.g. poisoning (herbicide, transition
 metal, carbon monoxide, and antibiotic toxicity). The present
 CC sequence is a human peptide that inhibits generation of reactive
 oxygen species (ROS).

SQ Sequence 12 AA;

Query Match 100.0%; Score 58; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e-05; Mismatches 0; Indels 0; Gaps 0;

Db 0y 1 AHKSEVAHRFK 11

2 AHKSEVAHRFK 12

RESULT 8
 ABB99709

ID ABB99709 standard; peptide; 12 AA.

XX

AC ABB99709;

XX

DT 28-MAR-2003 (first entry)

XX

DE Biopolymer marker indicative of congestive heart failure.

XX

KW Biopolymer marker; congestive heart failure.

XX

OS Homo sapiens.

XX

PN WO200288723-A2.

XX

PD 07-NOV-2002.

XX

PF 26-APR-2002; 2002WO-CA00611.

XX

PR 30-APR-2001; 2001US-0846347.

XX

PA (SYN) X PHARMA INC.

XX

PI Jackowski G, Thatcher B, Vrees T, Yantha J, Marshall J;

XX

DR WPI; 2003-111906/10.

XX

New biopolymer marker for use in diagnostic assays for the detection or characterization of a particular disease state, especially congestive heart failure.

XX

Claim 1; Page 28; 28pp; English.

XX

The present sequence represents a biopolymer marker which is indicative of congestive heart failure. The biopolymer marker is used for evidencing and categorizing a disease state. It is used in an assay diagnostic kit and in diagnosing, determining risk-assessment, and identifying therapeutic avenues related to a disease state, such as congestive heart failure. Controlling the presence or absence of the biopolymer marker is used to regulate a disease state.

SQ Sequence 12 AA;

Query Match 100.0%; Score 58; DB 24; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e-05; Mismatches 0; Indels 0; Gaps 0;

Db 0y 1 AHKSEVAHRFK 11

2 AHKSEVAHRFK 12

RESULT 9

AAW74538
 ID AAW74538 standard; peptide; 13 AA.
 XX
 AC AAW74538;
 XX
 DT 02-DEC-1998 (first entry)
 XX
 DE Human serum albumin fragment.

XX
 KW Human; zonula occludens toxin receptor; ZOT receptor;
 KW antagonist; toxin; anti-inflammatory drug; antibody;
 KW gastrointestinal; inflammatory bowel disease; food allergy;
 KW protein loosing enteropathy; Coeliac disease; adsorption enhancer;

XX
 OS Homo sapiens.

XX
 PN WO9837096-A1.

XX
 PD 27-AUG-1998.

XX
 PF 18-FEB-1998; 98WO-US02257.

XX
 PR 17-FEB-1998; 98US-0024198.

XX
 PR 20-FEB-1997; 97US-0803364.

XX
 PA (YMA-) UNIV MARYLAND BALTIMORE.

XX
 PI Fassano A;

XX
 DR WPI; 1998-467493/40.

XX
 PT New zonula occludens toxin receptors - for identifying receptor antagonists which can be used as anti-inflammatory drugs and agonists useful as intestinal/nasal adsorption enhancers

XX
 PS Example 7; Page 49; 68pp; English.

XX
 CC This is the amino acid sequence of a fragment of the human serum

CC albumin used in the method of the invention where human zonula

CC occludens toxin (ZOT) receptor is used. The ZOT receptor is used

CC as capture ligand in affinity assays for agonists and antagonists

CC of the toxin. Antagonists of ZOT are specifically useful as

CC anti-inflammatory drugs in the treatment of gastrointestinal

CC conditions that display an increased intestinal permeability, e.g.

CC inflammatory bowel diseases, protein loosing enteropathy, food

CC allergies, and coeliac disease. Agonists of ZOT can rapidly open

CC tight junctions in a reversible and reproducible manner and are

CC useful as intestinal or nasal adsorption enhancers. The receptors

CC are also useful for generating monoclonal or polyclonal antibodies

CC (using conventional techniques), and to purify ZOT and fusion

CC proteins comprising ZOT by affinity chromatography.

XX
 SQ Sequence 13 AA;

XX
 Query Match 100.0%; Score 58; DB 19; Length 13;

XX
 Best Local Similarity 100.0%; Pred. No. 8.7e-05;

XX
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 Db QY 1 AHKSEVAHRFK 11

1 AHKSEVAHRFK 11

2 AHKSEVAHRFK 12

XX
 DT 13-MAY-2003 (first entry)

XX
 DE Congestive heart failure disease specific marker #2.

AAW74538
 ID AAW74538 standard; peptide; 13 AA.

XX
 AC AAW74538;

XX
 DT 02-DEC-1998 (first entry)

XX
 DE Human serum albumin fragment.

XX
 KW Human; zonula occludens toxin receptor; ZOT receptor;

KW antagonist; toxin; anti-inflammatory drug; antibody;

KW gastrointestinal; inflammatory bowel disease; food allergy;

KW protein loosing enteropathy; Coeliac disease; adsorption enhancer;

XX
 OS Homo sapiens.

XX
 PN WO9837096-A1.

XX
 PD 27-AUG-1998.

XX
 PF 18-FEB-1998; 98WO-US02257.

XX
 PR 17-FEB-1998; 98US-0024198.

XX
 PR 20-FEB-1997; 97US-0803364.

XX
 PA (YMA-) UNIV MARYLAND BALTIMORE.

XX
 PI Fassano A;

XX
 DR WPI; 1998-467493/40.

XX
 PT New zonula occludens toxin receptors - for identifying receptor

PT antagonists which can be used as anti-inflammatory drugs and

PT agonists useful as intestinal/nasal adsorption enhancers

XX
 PS Example 7; Page 49; 68pp; English.

XX
 CC This is the amino acid sequence of a fragment of the human serum

CC albumin used in the method of the invention where human zonula

CC occludens toxin (ZOT) receptor is used. The ZOT receptor is used

CC as capture ligand in affinity assays for agonists and antagonists

CC of the toxin. Antagonists of ZOT are specifically useful as

CC anti-inflammatory drugs in the treatment of gastrointestinal

CC conditions that display an increased intestinal permeability, e.g.

CC inflammatory bowel diseases, protein loosing enteropathy, food

CC allergies, and coeliac disease. Agonists of ZOT can rapidly open

CC tight junctions in a reversible and reproducible manner and are

CC useful as intestinal or nasal adsorption enhancers. The receptors

CC are also useful for generating monoclonal or polyclonal antibodies

CC (using conventional techniques), and to purify ZOT and fusion

CC proteins comprising ZOT by affinity chromatography.

XX
 SQ Sequence 13 AA;

XX
 Query Match 100.0%; Score 58; DB 19; Length 13;

XX
 Best Local Similarity 100.0%; Pred. No. 8.7e-05;

XX
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 Db QY 1 AHKSEVAHRFK 11

1 AHKSEVAHRFK 11

2 AHKSEVAHRFK 12

XX
 DT 13-MAY-2003 (first entry)

XX
 DE Congestive heart failure disease specific marker #2.

RESULT 10

ABG75657

ID ABG75657

XX
 AC ABG75657;

XX
 DT 13-MAY-2003

(first entry)

XX
 DE Congestive heart failure disease specific marker #2.

XX Biopolymer marker; serum albumin; disease specific marker.
 KW congestive heart failure.
 XX Unidentified.

XX Location/Qualifiers
 Key Misc-difference 1
 /note= "Residue is optionally absent"
 FT Misc-difference 13
 /note= "Residue is optionally absent"

XX US2002160417-A1.
 XX PD 31-OCT-2002.
 XX PF 30-APR-2001; 2001US-0845726.
 XX PR 30-APR-2001; 2001US-0845726.
 XX PA (JACK) JACKOWSKI G.
 PA (STAN) STANTON E B.
 (THAT) THATCHER B.
 PA (VREE) VBEREES T.
 (YANT) YANTRA J.
 PA (MARS) MARSHALL J.
 XX PI Jackowski G, Stanton EB, Thatcher B, Vrees T, Yantha J;
 Marshall J;
 XX DR; 2003-246641/25.

Novel biopolymer marker such as serum albumin having specific molecular weight, useful in indicating disease state such as congestive heart failure -
 Disclosure: Fig 1; 10pp; English.

XX The invention relates to a biopolymer marker such as serum albumin having a molecular weight of about 1124 daltons, useful in indicating at least one particular disease state. The biopolymer marker is useful for indicating at least one particular disease state such as congestive heart failure and as an antigen in immunoassays for the detection of those individuals suffering from the disease known to be evidenced by the marker sequence. The biopolymer marker rapidly and accurately diagnoses a disease state such as congestive heart failure and allows physicians to identify asymptomatic patients before they develop the disease state. This sequence represents a congestive heart failure disease specific marker.

XX Sequence 13 AA;

Query Match 100.0%; Score 58; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 8.7e-05; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AHKSEVAHRFK 11
 ||||| | | | | | | |
 Db 2 AHKSEVAHRFK 12

XX DE Human serum albumin biopolymer marker peptide.
 XX FH Key
 FT Misc-difference 1 Location/Qualifiers
 FT /note= "Optionally absent"
 AAB12462 standard; Peptide: 20 AA.
 XX AC AAB12462;
 XX DT 25-OCT-2000 (first entry)
 DE Human albumin epitope peptide #1.
 XX KW Monoclonal antibody; hybridoma cell; immunoglobulin; IgG; fusion;
 RW human albumin; diabetic nephropathy; diagnosis.

XX OS Homo sapiens.
 XX PN JP20000139460-A.
 XX PD 23-MAY-2000.
 XX PF 02-NOV-1998; 98JP-0311677.
 XX PR 02-NOV-1998; 98JP-0311677.
 XX PA (TOYW) TOYOTA CHUO KENKYUSHO KK.
 PA (AISE) AISIN SEIKI KK.
 XX WPI; 2000-433935/38.
 XX PT Hybridoma cells for preparation of IgG monoclonal antibody capable of rapid reaction with human albumin for diagnosis of diabetic nephropathy.
 PT -
 XX DR 2000-433935/38.
 XX PS Example: Fig 1; 11pp; Japanese.
 XX CC The present invention describes hybridoma cells used for preparing an immunoglobulin G (IgG) monoclonal antibody capable of rapid reaction with human albumin. The hybridoma cells are prepared by fusion of mammal myeloma cells and spleen cells immunised with human serum albumin, and producing IgG monoclonal antibody which rapidly react with human albumin. The monoclonal antibodies can be used in the diagnosis of diabetic nephropathy. The present sequence represents a human albumin epitope peptide sequence which is used in an example from the present invention.
 XX SQ Sequence 20 AA;
 Query Match 100.0%; Score 58; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.00014; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0;
 Qy 1 AHKSEVAHRFK 11
 ||||| | | | | | | |
 Db 3 AHKSEVAHRFK 13

RESULT 12
 ABG75942
 ID ABG75942 standard; peptide; 26 AA.
 XX AC ABG75942;
 XX DT 08-MAY-2003 (first entry)
 XX DE Human serum albumin biopolymer marker peptide.
 XX FH Key
 FT Misc-difference 1 Location/Qualifiers
 FT /note= "Optionally absent"
 AAB12462 standard; Peptide: 20 AA.
 XX AC AAB12462;
 XX DT 25-OCT-2000 (first entry)
 DE Human albumin epitope peptide #1.
 XX KW Surface Enhanced Laser Desorption Ionization mass spectrometry;
 KW time-of-flight detection procedure; complement system disease;
 KW syndrome X; insulin resistance; hyperinsulinaemia.
 XX OS Homo sapiens.
 XX FH Key
 FT Misc-difference 1 Location/Qualifiers
 FT /note= "Optionally absent"
 AAB12462 standard; Peptide: 20 AA.
 XX AC AAB12462;
 XX DT 25-OCT-2000 (first entry)
 DE Human albumin epitope peptide #1.
 XX KW Monoclonal antibody; hybridoma cell; immunoglobulin; IgG; fusion;
 RW human albumin; diabetic nephropathy; diagnosis.

XX PN US2002160531-A1.
 XX PD 31-OCT-2002.
 XX PR 30-APR-2001; 2001US-0846328.

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you only*

XX PR 30-APR-2001; 2001US-0846328.
XX DR WPI; 2003-246645/25.

PA (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANNA J.
PA (VREE/) VREES T.
XX

PI JACKowski G., Thatcher B., Marshall J., Yantha J., Vrees T;
XX DR WPI; 2003-361743/34.

PT A new biopolymer marker useful in indicating a particular disease state -
particular insulin resistance -
Disclosure; Fig 1; 10pp; English.

XX The invention describes a biopolymer marker useful in indicating at least one particular disease state. Biopolymer markers are identified using Surface Enhanced Laser Desorption Ionization (SELDI) mass spectrometry and time-of-flight detection procedures. The markers are useful for indicating e.g. complement system diseases and syndrome X, characterised by the clustering of insulin resistance and hyperinsulinaemia. This is the amino acid sequence of a human serum albumin biopolymer marker useful for indicating insulin resistance.

XX Sequence 26 AA;

Query	Match	Score	DB	Length	Indels	Gaps	0;
Qy	1 AHKSEVAHRFK 11 3 AHKSEVAHRFK 13	100.0%; 100.0%; 0;	24; 24; 0;	26;	0;	0;	0;

DB

RESULT 13
ABU09223
ID ABU09223 standard; peptide; 28 AA.
XX AC ABU09223;
XX DT 13-JUN-2003 (first entry).
XX DE Serum albumin insulin resistance disease specific marker.
XX KW Human; insulin resistance; syndrome X; obesity; hyperinsulinaemia; complement system disease; serum albumin; biopolymer marker; lipaemia; glucose intolerance; blood coagulation abnormality; hyperlipidaemia; KW albumuria; kidney failure; stroke; hypertension; diabetes; heart failure.
XX OS Homo sapiens.
XX Key Location/Qualifiers
PH Region 2..27
PT /note- "Specifically claimed in claim 1"
XX PN US2003161177-A1.
XX PD 31-OCT-2002.
XX PF 30-APR-2001; 2001US-0846329.
XX PR 30-APR-2001; 2001US-0846329.
XX PA (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANNA J.
PA (VREE/) VREES T.
XX PS

XX PI JACKowski G., Thatcher B., Marshall J., Yantha J., Vrees T;
XX DR WPI; 2003-361743/34.
XX PT Serum albumin biopolymer marker having specific molecular weight -
Indicates at least one particular disease state -
Disclosure; Fig 1; 10pp; English.

XX The invention relates to a serum albumin biopolymer marker having a molecular weight of 2937 daltons which indicates at least one particular disease state. The biopolymer marker is useful for indicating at least one particular disease state, e.g. insulin resistance. Also for diseases associated with the complement system and syndrome X such as obesity, hyperinsulinaemia, lipaemia, glucose intolerance, blood coagulation abnormalities, hyperlipidaemia, albuminuria, hyperuricaemia, kidney failure, stroke, hypertension, diabetes and heart failure. The biopolymer marker enables a diagnostician to gain the ability to characterise either the presence or absence of the disease state relative to recognition of the presence and/or the absence of the biopolymer. The present sequence represents the amino acid sequence of the serum albumin insulin resistance disease specific marker.

XX SQ Sequence 28 AA;

Query	Match	Score	DB	Length	Indels	Gaps	0;
Qy	1 AHKSEVAHRFK 11 3 AHKSEVAHRFK 13	100.0%; 100.0%; 0;	24; 24; 0;	28;	0;	0;	0;

DB

RESULT 14
AA01161
ID AA011631 standard; Protein; 113 AA.
XX AC AA011631;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 25523.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US04927.
XX PR 28-FEB-2000; 2000US-0515126.
XX PR 18-MAY-2000; 2000US-0577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-514838/56.
XX N-PSDB; AA191562.
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
XX PS Claim 20; SEQ ID NO 25523; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity eliciting to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haemopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 113 AA;

Query Match	100.0%	Score 58;	DB 22;	Length 113;
Best Local Similarity	100.0%	Pred. No.	0.0011;	
Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 AHKSEVAHRFK 11

Db 30 AHKSEVAHRFK 40

RESULT 15

AA002642

ID AA002642 standard; Protein: 116 AA.

XX

AC AA002642;

XX

DT 06-NOV-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 16534.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US04927.

XX PR 28-FEB-2000; 2000US-0515126.

XX PR 18-MAY-2000; 2000US-0577499.

XX PA (HYSEQ-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR 2001-514830/56.

DR N-PSDB; AAI82573.

XX PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX PS Claim 20; SEQ ID NO 16534; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity eliciting to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haemopoiesis regulating